

OM protein - protein search, using sw model

Run on: October 4, 2004, 18:37:13 ; Search time 52.2391 Seconds
(without alignments)
48.679 Million cell updates/sec

Title: US-10-048-209-2

Perfect score: 52

Sequence: 1 KQVTSIHG 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A.Geneseq_29Jan04:*

1: geneseq1980s:*

2: geneseq1990s:*

3: geneseq2000s:*

4: geneseq2001s:*

5: geneseq2002s:*

6: geneseq2003as:*

7: geneseq2003bs:*

8: geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	52	100.0	11	4 AAB67792	Aab67792 Cytoplasm
2	52	100.0	12	4 AAB67793	Aab67793 Cytoplasm
3	52	100.0	13	4 AAB67794	Aab67794 Cytoplasm
4	52	100.0	15	4 AAB67798	Aab67798 Cytoplasm
5	52	100.0	19	7 ADC49255	Adc49255 Human inh
6	52	100.0	26	2 AAR58933	Aar58933 KQVTSI-ad
7	52	100.0	32	6 AAO19883	Aao19883 Human amy
8	52	100.0	33	7 ADC49254	Adc49254 Human inh
9	52	100.0	41	4 AAM16658	Aam16658 Peptide #

10	52	100.0	41	4 ABB35642	Abb35642 Peptide #
11	52	100.0	41	4 AAM29142	Aam29142 Peptide #
12	52	100.0	41	4 ABB30475	Abb30475 Peptide #
13	52	100.0	41	4 ABB21071	Abb21071 Protein #
14	52	100.0	41	4 AAM56458	Aam56458 Human bra
15	52	100.0	41	4 AAM43374	Aam43374 Peptide #
16	52	100.0	41	5 ABB38416	Abb38416 Human pep
17	52	100.0	44	2 AAR53985	Aar53985 Human ALZ
18	52	100.0	47	2 AAR58917	Aar58917 Cytoplasm
19	52	100.0	47	2 AAW26395	Aaw26395 Amyloid p
20	52	100.0	47	2 AAW26402	Aaw26402 Amyloid p
21	52	100.0	47	2 AAW26400	Aaw26400 Amyloid p
22	52	100.0	47	2 AAW26403	Aaw26403 Amyloid p
23	52	100.0	47	2 AAW26399	Aaw26399 Amyloid p
24	52	100.0	47	2 AAW26401	Aaw26401 Amyloid p
25	52	100.0	47	2 AAW26520	Aaw26520 Amyloid p
26	52	100.0	47	2 AAW26518	Aaw26518 Amyloid p
27	52	100.0	47	2 AAW26521	Aaw26521 Amyloid p
28	52	100.0	47	2 AAW26519	Aaw26519 Amyloid p
29	52	100.0	47	2 AAW26513	Aaw26513 Amyloid p
30	52	100.0	47	2 AAW26517	Aaw26517 Amyloid p
31	52	100.0	47	2 AAW42984	Aaw42984 APP isofo
32	52	100.0	47	2 AAW42986	Aaw42986 APP isofo
33	52	100.0	47	2 AAW42987	Aaw42987 APP isofo
34	52	100.0	47	2 AAW42983	Aaw42983 APP isofo
35	52	100.0	47	2 AAW42985	Aaw42985 APP isofo
36	52	100.0	47	2 AAW44755	Aaw44755 APP-REP 7
37	52	100.0	47	2 AAW44753	Aaw44753 APP-REP 7
38	52	100.0	47	2 AAW44756	Aaw44756 APP-REP 7
39	52	100.0	47	2 AAW44754	Aaw44754 APP-REP 7
40	52	100.0	47	2 AAW44757	Aaw44757 APP-REP 7
41	52	100.0	47	2 AAW44274	Aaw44274 Amyloid p
42	52	100.0	47	2 AAB67791	Aab67791 Cytoplasm
43	52	100.0	47	4 ADC49250	Adc49250 Human inh
44	52	100.0	47	7 ADC49250	Adc49250 Human inh
45	52	100.0	47	7 ADC49249	Adc49249 Inhibitor

ALIGNMENTS

RESULT 1
AAB67792
ID AAB67792 standard; peptide; 11 AA.
XX
AC AAB67792;
XX
DT 11-JUN-2001 (first entry)
XX
DE Cytoplasmic domain of the amyloid protein precursor (APP).
XX
KW Amyloid protein precursor; APP; apoptosis; cancer; Alzheimer's disease.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 1

FT /note= "this residue represents an internalisation
 FT peptide such as the sequence given in AAB67795"
 FT Misc-difference 11
 FT /note= "this residue represents V, W, VVE, VVEV, VVEVD"
 FT
 XX PN WO200109170-A1.
 XX PD 08-FEB-2001.
 XX PF 28-JUL-2000; 2000WO-FR002174.
 XX PR 30-JUL-1999; 99FR-00009929.
 XX PA (CNRS) CNRS CENT NAT RECH SCI.
 XX PI Allinquant B, Prochiantz A;
 XX DR WPI; 2001-257398/26.
 XX PT Peptides derived from the cytoplasmic domain of the amyloid protein
 PT precursor, useful in the treatment of cancer and Alzheimer's disease.
 XX PS Claim 1; Page 13; 28pp; French.
 XX CC The present sequence represents a peptide derived from the cytoplasmic
 CC domain of the human amyloid protein precursor (APP). APP peptides derived
 CC from the cytoplasmic domain, and containing the membrane domain
 CC juxtaposed to the cytoplasmic domain of APP are useful for selecting and
 CC screening products capable of inhibiting apoptosis. The peptides are
 CC useful in the treatment of cancer and Alzheimer's disease
 XX SQ Sequence 11 AA;
 Query Match 100.0%; Score 52; DB 4; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.0033;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KQYTSIHG 9
 | | | | | | | | | |
 Db 2 KQYTSIHG 10
 RESULT 2
 AAB67793
 ID AAB67793 standard; peptide; 12 AA.
 XX AC AAB67793;
 XX DT 11-JUN-2001 (first entry)
 XX DE Cytoplasmic domain of the amyloid protein precursor (APP).
 XX KW Amyloid protein precursor; APP; apoptosis; cancer; Alzheimer's disease.
 XX OS Homo sapiens.
 XX FH Key Location/Qualifiers

FT Misc-difference 1
 FT /note= "this residue represents an internalisation
 FT peptide such as the sequence given in AAB67795"
 FT Misc-difference 12
 FT /note= "this residue represents V, W, VVE, VVEV, VVEVD"
 FT
 XX PN WO200109170-A1.
 XX PD 08-FEB-2001.
 XX PF 28-JUL-2000; 2000WO-FR002174.
 XX PR 30-JUL-1999; 99FR-00009929.
 XX PA (CNRS) CNRS CENT NAT RECH SCI.
 XX PI Allinquant B, Prochiantz A;
 XX DR WPI; 2001-257398/26.
 XX PT Peptides derived from the cytoplasmic domain of the amyloid protein
 PT precursor, useful in the treatment of cancer and Alzheimer's disease.
 XX PS Claim 1; Page 13; 28pp; French.
 XX CC The present sequence represents a peptide derived from the cytoplasmic
 CC domain of the human amyloid protein precursor (APP). APP peptides derived
 CC from the cytoplasmic domain, and containing the membrane domain
 CC juxtaposed to the cytoplasmic domain of APP are useful for selecting and
 CC screening products capable of inhibiting apoptosis. The peptides are
 CC useful in the treatment of cancer and Alzheimer's disease
 XX SQ Sequence 12 AA;
 Query Match 100.0%; Score 52; DB 4; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.0036;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KQYTSIHG 9
 | | | | | | | | | |
 Db 3 KQYTSIHG 11
 RESULT 3
 AAB67794
 ID AAB67794 standard; peptide; 13 AA.
 XX AC AAB67794;
 XX DT 11-JUN-2001 (first entry)
 XX DE Cytoplasmic domain of the amyloid protein precursor (APP).
 XX KW Amyloid protein precursor; APP; apoptosis; cancer; Alzheimer's disease.
 XX OS Homo sapiens.
 XX FH Key

FH Key Location/Qualifiers
 FT Misc-difference 1 /note= "this residue represents an internalisation
 FT peptide such as the sequence given in AAB67795"
 FT Misc-difference 13
 FT /note= "this residue represents V, VV, VVE, VVEV, VVEVD"
 XX
 PN WO200109170-A1.
 XX
 PD 08-FEB-2001.
 XX
 XX 28-JUL-2000; 2000WO-FR002174.
 XX
 PR 30-JUL-1999; 99FR-00009929.
 XX
 PA (CNRS) CNRS CENT NAT RECH SCI.
 XX
 PI Allinquant B, Prochiantz A;
 XX
 DR WPI; 2001-257398/26.
 XX
 XX Peptides derived from the cytoplasmic domain of the amyloid protein
 PT precursor, useful in the treatment of cancer and Alzheimer's disease.
 XX
 PS Claim 1; Page 13; 28pp; French.
 XX
 CC The present sequence represents a peptide derived from the cytoplasmic
 CC domain of the human amyloid protein precursor (APP). APP peptides derived
 CC from the cytoplasmic domain, and containing the membrane domain
 CC juxtaposed to the cytoplasmic domain of APP are useful for selecting and
 CC screening products capable of inhibiting apoptosis. The peptides are
 CC useful in the treatment of cancer and Alzheimer's disease
 XX
 SQ Sequence 13 AA;
 Query Match 100.0%; Score 52; DB 4; Length 13;
 Best Local Similarity 100.0%; Pred. No. 0.0039;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KQYTSIHG 9
 DB 4 KQYTSIHG 12
 RESULT 4
 AAB67798
 ID AAB67798 standard; peptide; 15 AA.
 XX
 AC AAB67798;
 XX
 DT 11-JUN-2001 (first entry)
 XX
 DE Cytoplasmic domain of the amyloid protein precursor (APP).
 XX
 KW Amyloid protein precursor; APP; apoptosis; cancer; Alzheimer's disease.
 XX
 OS Homo sapiens.

XX WO200109170-A1.
 PN
 PD 08-FEB-2001.
 XX
 XX 28-JUL-2000; 2000WO-FR002174.
 XX
 PR 30-JUL-1999; 99FR-00009929.
 XX
 PA (CNRS) CNRS CENT NAT RECH SCI.
 XX
 PI Allinquant B, Prochiantz A;
 XX
 DR WPI; 2001-257398/26.
 XX
 XX Peptides derived from the cytoplasmic domain of the amyloid protein
 PT precursor, useful in the treatment of cancer and Alzheimer's disease.
 XX
 PS Disclosure; Page 2; 28pp; French.
 XX
 CC The present sequence represents a peptide derived from the cytoplasmic
 CC domain of the human amyloid protein precursor (APP). APP peptides derived
 CC from the cytoplasmic domain, and containing the membrane domain
 CC juxtaposed to the cytoplasmic domain of APP are useful for selecting and
 CC screening products capable of inhibiting apoptosis. The peptides are
 CC useful in the treatment of cancer and Alzheimer's disease
 XX
 SQ Sequence 15 AA;
 Query Match 100.0%; Score 52; DB 4; Length 15;
 Best Local Similarity 100.0%; Pred. No. 0.0046;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KQYTSIHG 9
 DB 3 KQYTSIHG 11
 RESULT 5
 ADC49255
 ID ADC49255 standard; protein; 19 AA.
 XX
 AC ADC49255;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Human inhibitor of metabolic degradation of APP variant #4.
 XX
 KW human; inhibitory factor; metabolic degradation of APP;
 KW amyloid precursor protein; Alzheimer's disease; mutant; mutetin.
 XX
 OS Homo sapiens.
 XX
 PN JP2002360252-A.
 XX
 PD 17-DEC-2002.
 XX

PF	27-APR-2001; 2001JP-00133178.
XX	
XX	
PR	27-APR-2001; 2001JP-00133178.
XX	
XX	(SUZU/) SUZUKI T.
PA	(SUMI) SUMITOMO SEIYAKU KK.
PA	
XX	
DR	WPI; 2003-516151/49.
XX	
XX	An inhibitory factor of metabolic degradation of amyloid precursor protein (APP) which inhibits formation of beta-amyloid, useful in the treatment of Alzheimer's disease.
PT	
PT	
PS	Disclosure; SEQ ID NO 15; 33pp; Japanese.
XX	
XX	The invention relates to an inhibitory factor of metabolic degradation of APP. The factor is useful in the treatment of Alzheimer's disease. The present sequence is used in the exemplification of the invention.
CC	
CC	
XX	
SQ	Sequence 19 AA;
	Query Match 100.0%; Score 52; DB 7; Length 19;
	Best Local Similarity 100.0%; Pred. No. 0.006;
	Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 KQYTSIHGG 9
DB	3 KQYTSIHGG 11
RESULT 6	
AAR58933	
ID	AAR58933 standard; peptide; 26 AA:
XX	
AC	AAR58933;
XX	
DT	25-MAR-2003 (revised)
DT	15-APR-1995 (first entry)
XX	
DE	KQYTSI-added variant of His657-Lys676 region of human cytoplasmic amyloid precursor protein APP695.
XX	
KW	Amyloid precursor protein; isoform APP 695; beta amyloid; peptide 20; Go;
XW	GIP Binding protein; couplone region; Alzheimer's disease.
XX	
OS	Homo sapiens.
XX	
PN	W09419692-A1.
XX	
PD	01-SEP-1994.
XX	
PF	17-FEB-1994; 94WO-US001712.
XX	
FR	18-FEB-1993; 93US-00019208.
XX	
PA	(GEO) GEN HOSPITAL CORP.
XX	
XX	

Nishimoto I;
XX
XX
WPI; 1994-294486/36.
Identifying cpds. useful for treating or preventing Alzheimer's disease - by determining whether it interferes with the association of the couplone portion of amyloid precursor protein to G polypeptide.
XX
XX
Disclosure; Page 34; 71pp; English.
XX
Beta amyloid is synthesised as part of a larger protein referred to as amyloid precursor protein (APP), which has a number of isoforms in humans, including APP695 and APP770. The amino terminal of beta amyloid is generated by cleavage of a peptide bond of APP which in APP695 lies between Met596 and Asp597. APP forms a complex with Go, a GTP-binding protein (or "G protein") in brain. The cytoplasmic APP695 sequence His657-Lys676 (AAR58913) possesses a specific Go-activating function, and is necessary for complex formation of this APP with Go. This sequence (AAR58913), sometimes referred to as the "couplone" region of APP, is completely conserved in APP751 and App770, as well as in mouse App695, and suggests that abnormal APP-Go signalling is involved in the Alzheimer's disease process. This peptide is referred to a 'peptide 20'. Variants of peptide 20 are given in AAR58930-R58934. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 26 AA;
Query Match 100.0%; Score 52; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.0084;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KQYTSIHGG 9
| | | | | | | | | |
DB 1 KQYTSIHGG 9

RESULT 7
AAO19863
ID AAO19863 standard; peptide; 32 AA.
XX
AC AAO19863;
XX
DT 11-AUG-2003 (first entry)
XX
DE Human amyloid precursor protein APP immunogenic peptide #3.
XX
KW Human; APP; amyloid precursor protein; immunogen; Alzheimer's disease;
XW high-throughput screening; neuroprotective; nootropic; antiparkinsonian.
XX
OS Homo sapiens.
XX
PN WC2003001881-A2.
XX
PD 09-JAN-2003.
XX
PF 26-JUN-2002; 2002WO-US020267.
XX

PF		27-APR-2001; 2001JP-00133178.
XX		
XPR		27-APR-2001; 2001JP-00133178.
XX		
XX	(SUZU/)	SUZUKI T.
PPA	(SUMJ)	SUMITOMO SEIYAKU KK.
XX		
XX	WPI;	2003-516151/49.
DR		
XX		
XX	An inhibitory factor of metabolic degradation of amyloid precursor	
PPT	protein (APP) which inhibits formation of beta-amyloid, useful in the	
PPT	treatment of Alzheimer's disease.	
PT		
XX		
PS	Disclosure; SEQ ID NO 15; 33pp; Japanese.	
XX		
CC	The invention relates to an inhibitory factor of metabolic degradation of	
CC	APP. The factor is useful in the treatment of Alzheimer's disease. The	
CC	present sequence is used in the exemplification of the invention.	
XX		
XX	Sequence 19 AA;	
SQ		
	Query Match	100.0%; Score 52; DB 7; Length 19;
	Best Local Similarity	100.0%; Pred. No. 0.006;
	Matches	9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 KQYTSIHGG 9	
DB	3 KQYTSIHGG 11	
RESULT 6		
AAAR58933		
ID	AAAR58933 standard; peptide; 26 AA:	
XX	AAAR58933;	
XX		
DT	25-MAR-2003 (revised)	
DT	15-APR-1995 (first entry)	
XX		
DE	KQYTSI-added variant of His657-Lys676 region of human cytoplasmic amyloid	
DE	precursor protein APP695.	
XX		
KW	Amyloid precursor protein; isoform APP 695; beta amyloid; peptide 20; Go;	
KW	GFP binding protein; cloneone region; Alzheimer's disease.	
XX		
OS	Homo sapiens.	
XX		
PN	W09419692-A1.	
XX		
PD	01-SEP-1994.	
XX		
XX		
PF	17-FEB-1994; 94WO-US001712.	
XX		
XX	18-FEB-1993; 93US-00019208.	
PA	(GHEO) GEN HOSPITAL CORP.	
XX		
XX		

PR 26-JUN-2001; 2001US-0300959P.
 XX (NYME-) NEW YORK STATE OFFICE MENTAL HEALTH.
 XX Mathews PM, Nixon RA, Schmidt SD, Jiang Y;
 XX WPI; 2003-210182/20.
 DR
 XX Identifying compounds that modulates the generation of metabolites
 PT associated with a disease or disorder, for treating e.g. Alzheimer's
 PT disease by determining levels of a cellular component protein, or its
 PT conformation state.
 XX
 PS Example 1; Page 29; 69pp; English.
 CC The present invention relates to a method of identifying compounds that
 CC modulate the generation of one or more metabolites associated with a
 CC disease or disorder comprising determining levels of a cellular component
 CC protein or a conformation state of a cellular precursor protein. In
 CC particular, the method can be used to determine levels of amyloid
 CC precursor protein (APP), which is associated with Alzheimer's disease. It
 CC is also useful for identifying compounds as drugs for treating diseases
 CC or disorders associated with metabolic and/or proteolytic pathways, e.g.
 CC Alzheimer's disease, Parkinson's disease, Huntington's disease, lysosomal
 CC storage disorders, prion diseases, the tau-based neurodegenerative
 CC disorders, and other non-AD amyloidoses. The present sequence is an
 CC immunogenic portion of human APP
 XX
 XX Sequence 32 AA;
 SQ
 Query Match 100.0%; Score 52; DB 6; Length 32;
 Best Local Similarity 100.0%; Pred. No. 0.011;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KQYTSIHG 9
 DB 7 KQYTSIHG 15
 XX
 XX
 RESULT 8
 ADC49254
 ID ADC49254 standard; protein; 33 AA.
 XX
 XX ADC49254;
 XX
 XX 18-DEC-2003 (first entry)
 XX Human inhibitor of metabolic degradation of APP variant #3.
 XX human; inhibitory factor; metabolic degradation of APP;
 KW amyloid precursor protein; Alzheimer's disease; mutant; mutain.
 XX Homo sapiens.
 OS
 XX JP2002360252-A.
 PN
 XX 17-DEC-2002.
 PD

XX 27-APR-2001; 2001JP-00133178.
 PF
 XX 27-APR-2001; 2001JP-00133178.
 PR
 XX (SUZU) SUZUKI T.
 PA (SUMI) SUMITOMO SEIVAKU KK.
 PA
 XX WPI; 2003-516151/49.
 DR
 XX An inhibitory factor of metabolic degradation of amyloid precursor
 PT protein (APP) which inhibits formation of beta-amyloid, useful in the
 PT treatment of Alzheimer's disease.
 PT
 XX Disclosure; SEQ ID NO 14; 33pp; Japanese.
 PS
 XX The invention relates to an inhibitory factor of metabolic degradation of
 CC APP. The factor is useful in the treatment of Alzheimer's disease. The
 CC present sequence is used in the exemplification of the invention.
 CC
 XX Sequence 33 AA;
 SQ
 Query Match 100.0%; Score 52; DB 7; Length 33;
 Best Local Similarity 100.0%; Pred. No. 0.011;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KQYTSIHG 9
 DB 3 KQYTSIHG 11
 XX
 RESULT 9
 AAM16658
 ID AAM16658 standard; protein; 41 AA.
 XX
 XX AAM16658;
 AC
 XX 12-OCT-2001 (first entry)
 DT
 XX Peptide #3052 encoded by probe for measuring cervical gene expression.
 DE
 XX Probe; human; microarray; gene expression; cervical epithelial cell;
 KW cervical cancer.
 KW
 XX Homo sapiens.
 OS
 XX WO200157278-A2.
 PN
 XX 09-AUG-2001.
 PD
 XX 30-JAN-2001; 2001WO-US000670.
 PF
 XX 04-FEB-2000; 2000US-0180312P.
 PR
 XX 26-MAY-2000; 2000US-0207456P.
 PR
 XX 30-JUN-2000; 2000US-00608408.
 PR
 XX 03-AUG-2000; 2000US-00632366.
 PR
 XX 21-SEP-2000; 2000US-0234687P.
 PR

PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX
 DR WPI; 2001-488901/53.
 XX
 PT Human genome-derived single exon nucleic acid probes useful for analyzing
 PT gene expression in human cervical epithelial cells.
 XX
 PS Claim 27; SEQ ID NO 21484; 487pp; English.
 XX
 CC The present invention relates to human single exon nucleic acid probes
 CC (SENPs: see ARI0065-AA128459). The present sequence is a peptide encoded
 CC by one such probe. The SENPs are derived from human HeLa cells. The SENPs
 CC can be used to produce a single exon microarray, which can be used for
 CC measuring human gene expression in a sample derived from human cervical
 CC epithelial cells. By measuring gene expression, the probes are therefore
 CC useful in grading and/or staging of diseases of the cervix, notably
 CC cervical cancer. Note: The sequence data for this patent did not form
 CC part of the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 41 AA;
 Query Match 100.0%; Score 52; DB 4; Length 41;
 Best Local Similarity 100.0%; Pred. No. 0.014;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KQYTSIHG 9
 Db 30 KQYTSIHG 38
 RESULT 10
 ABB35642
 ID ABB35642 standard; peptide; 41 AA.
 XX
 AC ABB35642;
 XX
 DT 04-FEB-2002 (first entry)
 XX
 DE Peptide #3148 encoded by human foetal liver single exon probe.
 XX
 KW Human; foetal liver; gene expression; single exon nucleic acid probe.
 XX
 OS Homo sapiens.
 XX
 PN WO200157277-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 30-JAN-2001; 2001WO-US000669.
 XX
 PD 04-FEB-2000; 2000US-0180312P.
 PR

PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX
 DR WPI; 2001-483447/52.
 XX
 PT Human genome-derived single exon nucleic acid probes useful for analyzing
 PT gene expression in human fetal liver.
 XX
 PS Claim 27; SEQ ID NO 28277; 639pp + Sequence Listing; English.
 XX
 CC The invention relates to a single exon nucleic acid probe for measuring
 CC human gene expression in a sample derived from human foetal liver. The
 CC single exon nucleic acid probes may be used for predicting, measuring and
 CC displaying gene expression in samples derived from human fetal liver. The
 CC present sequence is a peptide encoded by a single exon nucleic acid probe
 CC of the invention. Note: The sequence data for this patent did not form
 CC part of the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 41 AA;
 Query Match 100.0%; Score 52; DB 4; Length 41;
 Best Local Similarity 100.0%; Pred. No. 0.014;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KQYTSIHG 9
 Db 30 KQYTSIHG 38
 RESULT 11
 AAM29142
 ID AAM29142 standard; protein; 41 AA.
 XX
 AC AAM29142;
 XX
 DT 17-OCT-2001 (first entry)
 XX
 DE Peptide #3179 encoded by probe for measuring placental gene expression.
 XX
 KW Probe; microarray; human; placenta; antenatal diagnosis;
 KW genetic disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200157272-A2.
 XX
 PD 09-AUG-2001.
 XX

PF 30-JAN-2001; 2001WO-US000663.
 XX 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 PA Penn SG, Hanzel DK, Chen W, Rank DR;
 PI WPI; 2001-488897/53.
 XX Human genome-derived single exon nucleic acid probes useful for analyzing
 PT gene expression in human placenta.
 PS Claim 27; SEQ ID NO 29411; 654pp; English.
 XX The present invention relates to single exon nucleic acid probes (SENPs;
 CC see AA131315-AA157546). The present sequence is a peptide encoded by one
 CC such probe. The probes are useful for producing a microarray for
 CC predicting, measuring and displaying gene expression in samples derived
 CC from human placenta. The probes are useful for antenatal diagnosis of
 CC human genetic disorders
 XX Sequence 41 AA;
 SQ
 Query Match 100.0%; Score 52; DB 4; Length 41;
 Best Local Similarity 100.0%; Pred. No. 0.014;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KQYTSIHGG 9
 Db 30 KQYTSIHGG 38
 RESULT 12
 ID ABB30475 standard; peptide; 41 AA.
 XX ABB30475;
 AC ABB30475;
 XX 01-FEB-2002 (first entry)
 DT Peptide #3126 encoded by breast cell single exon nucleic acid probe.
 DE Human; microarray; single exon probe; gene expression; breast; disease;
 XX cancer.
 KW Homo sapiens.
 XX
 OS W0200157271-A2.
 XX 09-AUG-2001.
 PN
 XX
 PD

XX 30-JAN-2001; 2001WO-US000662.
 PF 04-FEB-2000; 2000US-0180312P.
 XX 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 PA Penn SG, Hanzel DK, Chen W, Rank DR;
 PI WPI; 2001-496933/54.
 XX New spatially-addressable set of single exon nucleic acid probes, useful
 PT for measuring gene expression in sample derived from human breast,
 PT comprises number of single exon nucleic acid probes.
 PS Claim 27; SEQ ID NO 13443; 327pp + Sequence Listing; English.
 XX The invention relates to a spatially-addressable set of single exon
 CC nucleic acid probes for measuring gene expression in a sample derived
 CC from human breast and BT 474 cells. The method involves contacting the
 CC probes with a collection of detectably labelled nucleic acids derived
 CC from mRNA of human breast, and then measuring the label bound to each
 CC probe of the microarray. The probes are useful for verifying the
 CC expression of regions of genomic DNA predicted to encode proteins. They
 CC are useful for gene discovery, and for determining predisposition and/or
 CC assessing the toxicity of chemical agents on cells. The microarray of
 CC this invention presents a far greater diversity of probes for measuring
 CC gene expression, with far less bias than expressed sequence tag
 CC microarrays. The method is suitable for rapid production of functional
 CC information from genomic sequence. The present sequence is a peptide
 CC encoded by a single exon nucleic acid probe of the invention. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 41 AA;
 SQ
 Query Match 100.0%; Score 52; DB 4; Length 41;
 Best Local Similarity 100.0%; Pred. No. 0.014;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KQYTSIHGG 9
 Db 30 KQYTSIHGG 38
 RESULT 13
 ABB21071
 ID ABB21071 standard; protein; 41 AA.
 XX

AC ABB21071;
XX
DT 23-JAN-2002 (first entry)
XX
DE Protein #3070 encoded by probe for measuring heart cell gene expression.
XX
KW Human; gene expression; heart; microarray; vascular system;
KW cardiovascular disease; hypertension; cardiac arrhythmia;
KW congenital heart disease.
XX
OS Homo sapiens.
XX
PN WO200157274-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000666.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-488899/53.
XX
PT Single exon nucleic acid probes for analyzing gene expression in human hearts.
XX
PS Claim 15; SEQ ID NO 22841; 530pp; English.
XX
CC The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart (see CC ABA21535-ABA41305). The present sequence is a protein encoded by one such CC probe. The probes may be used for predicting, measuring and displaying CC gene expression in samples derived from the human heart via microarrays. CC By measuring gene expression, the probes are useful for predicting, CC diagnosing, grading, staging, monitoring and prognosing diseases of the CC human heart and vascular system e.g. cardiovascular disease, CC hypertension, cardiac arrhythmias and congenital heart disease. Note: The CC sequence data for this patent did not form part of the printed CC specification, but was obtained in electronic format directly from WIPO CC at ftp.wipo.int/pub/published_pot_sequences
XX
SQ Sequence 41 AA;
Query Match 100.0%; Score 52; DB 4; Length 41;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KQYTSIHG 9

Db 30 KQYTSIHG 38
|||||
RESULT 14
AAM56458
ID AAM56458 standard; protein; 41 AA.
XX
AC AAM56458;
XX
DT 05-NOV-2001 (first entry)
XX
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 28563.
XX
KW Human; brain expressed exon; gene expression analysis; probe; microarray;
KW Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.
XX
OS Homo sapiens.
XX
PN WO200157275-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000667.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-483446/52.
XX
PT Single exon nucleic acid probes for analyzing gene expression in human brains.
XX
PS Example 4; SEQ ID NO 28563; 650pp + Sequence Listing; English.
XX
CC The present invention provides a number of single exon nucleic acid CC probes which are derived from genomic sequences expressed in the human CC brain. They can be used to measure gene expression in brain cell samples, CC which may enable the diagnosis and improved treatment of nervous system CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, CC epilepsy and cancers. The present sequence is a protein encoded by one of CC the probes of the invention
XX
SQ Sequence 41 AA;
Query Match 100.0%; Score 52; DB 4; Length 41;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OM protein - protein search, using sw model

Run on: October 4, 2004, 18:45:55 ; Search time 13.3043 Seconds
(without alignments)
65.071 Million cell updates/sec

Title: US-10-048-209-2

Perfect score: 52

Sequence: 1 KQYTSIHG 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 78:**
1: pir1:**
2: pir2:**
3: pir3:**
4: pir4:**

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	52	100.0	82	PQ0438	Alzheimer's disease
2	52	100.0	695	A49795	Alzheimer's disease
3	52	100.0	695	A27485	Alzheimer's disease
4	52	100.0	695	S00550	Alzheimer's disease
5	52	100.0	770	Q8HUA4	Alzheimer's disease
6	49	94.2	747	JH0773	Alzheimer's disease
7	39	75.0	452	S58994	NADH2 dehydrogenas
8	38	73.1	488	S64140	hypothetical prote
9	37	71.2	442	A41661	ATP-dependent RNA
10	37	71.2	2584	T24158	hypothetical prote
11	37	71.2	2606	T24157	hypothetical prote
12	36	69.2	275	C75529	competence protein
13	36	69.2	412	T24023	hypothetical prote

14	36	69.2	443	2	T45332	probable dTDP-4-ke
15	35	67.3	150	2	P96924	flavodoxin (import
16	35	67.3	264	2	T15289	hypothetical prote
17	35	67.3	443	2	B39794	transcription fact
18	35	67.3	444	1	A39794	transcription fact
19	35	67.3	739	2	AG1667	phosphoribosylform
20	35	67.3	739	2	A11295	phosphoribosylform
21	35	67.3	1268	2	B88209	protein K02A2.6 (l
22	35	67.3	1313	2	T29193	hypothetical prote
23	34	65.4	99	2	B82524	hypothetical prote
24	34	65.4	254	2	T29556	hypothetical prote
25	34	65.4	332	2	T25779	hypothetical prote
26	34	65.4	393	2	C56592	hypothetical prote
27	34	65.4	410	2	AF1660	aminopeptidases ho
28	34	65.4	410	2	AG1288	aminopeptidases ho
29	34	65.4	637	2	H70535	hypothetical prote
30	34	65.4	784	2	T01139	Mutator-like trans
31	34	65.4	848	2	E85087	hypothetical prote
32	33	63.5	117	2	J70560	hemerythrin beta c
33	33	63.5	117	2	S50178	hemerythrin beta c
34	33	63.5	142	2	T10871	Y4KQ protein - Rhi
35	33	63.5	174	2	A47113	glucuronosyltransf
36	33	63.5	216	2	E97240	transcription regu
37	33	63.5	339	2	B34895	transcription fact
38	33	63.5	344	1	TXKL3	transcription fact
39	33	63.5	361	2	D83798	phosphoserine amin
40	33	63.5	406	2	S76307	hypothetical prote
41	33	63.5	434	2	C95362	probable aminopept
42	33	63.5	530	2	C47113	glucuronosyltransf
43	33	63.5	530	2	S66200	glucuronosyltransf
44	33	63.5	588	2	T04736	hypothetical prote
45	33	63.5	645	2	A83054	acetyl-coenzyme A

ALIGNMENTS

RESULT 1

PQ0438
Alzheimer's disease amyloid A4 protein precursor - rabbit (fragment)
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 30-Sep-1993 #sequence_revision 19-Oct-1995 #text_change 19-Oct-1995
C:Accession: PQ0438; C60045
R:Davidson, J.S.; West, R.L.; Kotikalapudi, P.; Maroun, L.E.
Biochem. Biophys. Res. Commun. 188, 905-911, 1992
A:Title: Sequence and methylation in the beta/A4 region of the rabbit amyloid
precursor protein gene.
A:Reference number: PQ0438; MUID:93075180; PMID:1445331
A:Accession: PQ0438
A:Molecule type: DNA
A:Residues: 1-82 <DAV>
A:Cross-references: GB:M83538; GB:M3657
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide
in dog, polar bear and five other mammals by cross-species polymerase chain
reaction analysis.

A/Reference number: A60045; MUID:92017079; PMID:1656157
A/Accession: C60045
A/Molecule type: mRNA
A/Residues: 12-68 <JOH>
A/Cross-references: EMBL:X56129
A/Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type
C/Keywords: alternative splicing; Alzheimer's disease; amyloid; Down's syndrome

Query Match 100.0%; Score 52; DB 2; Length 82;
Best Local Similarity 100.0%; Pred. No. 0.0047;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KQYTSIHG 9
|||||
Db 71 KQYTSIHG 79

RESULT 2
A27485
Alzheimer's disease amyloid beta protein precursor - crab-eating macaque
C/Species: Macaca fascicularis (crab-eating macaque)
C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C/Accession: A49795
R/Pedlisny, M.B.; Tolan, D.R.; Seikoe, D.J.
Am. J. Pathol. 138, 1423-1435, 1991
A/Title: Homology of the amyloid beta protein precursor in monkey and human supports a primate model for beta amyloidosis in Alzheimer's disease.
A/Reference number: A49795; MUID:91273117; PMID:1905108
A/Accession: A49795
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-695 <POD>
A/Cross-references: GB:M58727; NID:g342062; PIN:AAA36829.1; PID:g342063
C/Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type
C/Keywords: alternative splicing

Query Match 100.0%; Score 52; DB 1; Length 695;
Best Local Similarity 100.0%; Pred. No. 0.049;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KQYTSIHG 9
|||||
Db 651 KQYTSIHG 659

RESULT 3
A27485
Alzheimer's disease amyloid beta/A4 protein homolog precursor - mouse
N/Alternate names: proteinase nexin II
C/Species: Mus musculus (house mouse)
C/Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 13-Aug-1999
C/Accession: A27485; S19727; I49485
R/Yamada, T.; Sasaki, H.; Furuya, H.; Miyata, T.; Goto, I.; Sasaki, Y.
Biochem. Biophys. Res. Commun. 149, 665-671, 1987

A/Title: Complementary DNA for the mouse homolog of the human amyloid beta protein precursor.
A/Reference number: A27485; MUID:86106489; PMID:3322280
A/Accession: A27485
A/Molecule type: mRNA
A/Residues: 1-695 <YAN>
A/Cross-references: GB:M18373; NID:g191568; PIN:AAA37139.1; PID:g309085
A/Experimental source: brain
A/Experimental source: brain
Ride Strooper, B.; van Leuven, F.; van den Berghe, H.
Biochem. Biophys. Acta 1129, 141-143, 1991
A/Title: The amyloid beta protein precursor or proteinase nexin II from mouse is closer related to its human homolog than previously reported.
A/Reference number: S19727; MUID:92096438; PMID:1756177
A/Accession: S19727
A/Molecule type: mRNA
A/Residues: 1-210, 'G', 212-220, 'S', 222-396, 'A', 398-402, 'T', 404-448, 'A', 450-695
<STR>

A/Cross-references: EMBL:X59379
R/Izumi, R.; Yamada, T.; Yoshikai, S.; Sasaki, H.; Hattori, M.; Sasaki, Y.
Gene 112, 189-195, 1992
A/Title: Positive and negative regulatory elements for the expression of the Alzheimer's disease amyloid precursor-encoding gene in mouse.
A/Reference number: I49485; MUID:92209998; PMID:1555768
A/Accession: I49485
A/Status: translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-19 <RES>
A/Cross-references: GB:D10603; NID:g220328; PIN:BA01456.1; PID:g220329
C/Genetics:
A/Map position: 16C3
C/Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type
C/Keywords: alternative splicing; amyloid; transmembrane protein

Query Match 100.0%; Score 52; DB 2; Length 695;
Best Local Similarity 100.0%; Pred. No. 0.049;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KQYTSIHG 9
|||||
Db 651 KQYTSIHG 659

RESULT 4
S00550
Alzheimer's disease amyloid beta protein precursor - rat
N/Alternate names: beta-A4 amyloid protein
C/Species: Rattus norvegicus (Norway rat)
C/Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 13-Aug-1999
C/Accession: S00550; A41245; A39820; S46251
R/Shivers, B.D.; Hilbich, C.; Multhaup, G.; Salbaum, M.; Beyreuther, K.; Seeburg, P.H.
EMBO J. 7, 1365-1370, 1988
A/Title: Alzheimer's disease amyloidogenic glycoprotein: expression pattern in rat brain suggests a role in cell contact.
A/Reference number: S00550; MUID:86312583; PMID:2900758
A/Accession: S00550

A/Molecule type: mRNA
 A/Residues: 1-695 <SHI>
 A/Cross-references: EMBL:X07648; NID:g55616; PIDN:CAA30498.1; PID:g55617
 R/Schubert, D.; Schroeder, R.; LaCorbiere, M.; Saich, T.; Cole, G.
 Science 241, 223-226, 1988
 A/Title: Amyloid beta protein precursor is possibly a heparan sulfate
 proteoglycan core protein.
 A/Reference number: A41245; MJID:88264430; PMID:2969652
 A/Accession: A41245
 A/Molecule type: protein
 A/Residues: 18-37, 'X', 39-40, 'X', 42-44 <SCH>
 A/Note: evidence for heparan sulfate attachment
 R/Hesse, L.; Behner, D.; Masters, C.L.; Multhaup, G.
 FEBS Lett. 349, 109-116, 1994
 A/Title: The beta-A4 amyloid precursor protein binding to copper.
 A/Reference number: 846251; MJID:94320627; PMID:7913695
 A/Contents: annotation; copper binding sites
 A/Note: rat peptides were isolated but not sequenced
 R/Potempeka, A.; Styles, J.; Mehta, P.; Kim, K.S.; Miller, D.L.
 J. Biol. Chem. 266, 8464-8469, 1991
 A/Title: Purification and tissue level of the beta-amyloid peptide precursor of
 rat brain.
 A/Reference number: A39820; MJID:91217087; PMID:1673681
 A/Accession: A39820
 A/Status: preliminary
 A/Molecule type: Protein
 A/Residues: 18-32 <POT>
 A/Experimental source: Brain
 C/Comment: Deposition of amyloid protein as neurofibrillary tangles and/or
 plaques is characteristic of both Alzheimer's disease and Down's syndrome.
 C/Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type
 proteinase inhibitor homology
 C/Keywords: alternative splicing; amyloid; glycoprotein; transmembrane protein
 F:623-645/Domain: transmembrane #status predicted <TM>

 Query Match 100.0%; Score 52; DB 2; Length 695;
 Best Local Similarity 100.0%; Pred. No. 0.049;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 1 KQYTSIHG 9
 Db 651 KQYTSIHG 659

 RESULT 5
 QRHUA4
 Alzheimer's disease amyloid beta protein precursor [validated] - human
 N/Alternate names: Alzheimer's disease amyloid A4 protein; coagulation factor
 Xia inhibitor; proteinase nexin II (PN-II)
 N/Contains: amyloid beta protein long, plaque form; amyloid beta protein short,
 vascular form; amyloid protein precursor splice form APP(695); amyloid protein
 precursor splice form APP(751); amyloid protein precursor splice form APP(770)
 C/Species: Homo sapiens (man)
 C/Date: 30-Jun-1987 #sequence revision 28-Jul-1995 #text change 15-Sep-2000
 C/Accession: S02260; S05194; A32277; A33260; A35486; I39451; I39453;
 I59362; A44017; A44017; A03134; A29030; A47584; A47585; S02638; S00707; S00925;
 A38949; A30320; B30320; C30320; A31087; A24668; A28563; A29302; A60805; J10038;

S06121; A60355; A59011; A38384; S29076; S38252; S32539; S48148; S48692; S51186;
 S51185; S51184; S51183; A54238; I59075; I52250; S09010; S10737; S24127; S43044
 R/Lemair, H.G.; Salbaum, J.M.; Multhaup, G.; Kang, J.; Bayney, R.M.; Unterbeck,
 A.; Beyreuther, K.; Mueller-Hill, B.
 Nucleic Acids Res. 17, 517-522, 1989
 A/Title: The PreA4(695) precursor protein of Alzheimer's disease A4 amyloid is
 encoded by 16 exons.
 A/Reference number: S02260; MJID:89128427; PMID:2783775
 A/Accession: S02260
 A/Molecule type: DNA
 A/Residues: 1-288, 'V', 365-770 <LEM1>
 A/Cross-references: EMBL:X13466
 A/Note: alternative splice form APP(695)
 R/Lemair, H.G.
 submitted to the EMBL Data Library, November 1988
 A/Reference number: S05194
 A/Accession: S05194
 A/Molecule type: DNA
 A/Residues: 1-14, 'VM', 17-288, 'V', 365-770 <LEM2>
 A/Cross-references: EMBL:X13466; NID:g35598; PIDN:CAA31830.1; PID:g871360
 A/Note: alternative splice form APP(695)
 R/La Faudi, G.; Lahiri, D.K.; Salton, S.R.J.; Robakis, N.K.
 Biochem. Biophys. Res. Commun. 159, 297-304, 1989
 A/Title: Characterization of the 5'-end region and the first two exons of the
 beta-protein precursor gene.
 A/Reference number: A32277; MJID:89165870; PMID:2538123
 A/Accession: A32277
 A/Molecule type: DNA
 A/Residues: 1-75 <LAF>
 A/Cross-references: GB:M24546; GB:M24547; NID:g341202; PIDN:AA013654.1;
 PID:g316074
 R/Johnstone, E.M.; Chaney, M.O.; Moore, R.E.; Ward, K.E.; Norris, F.H.; Little,
 S.P.
 Biochem. Biophys. Res. Commun. 163, 1248-1255, 1989
 A/Title: Alzheimer's disease amyloid peptide is encoded by two exons and shows
 similarity to soybean trypsin inhibitor.
 A/Reference number: A33260; MJID:89392030; PMID:2675837
 A/Accession: A33260
 A/Molecule type: DNA
 A/Residues: 656-737 <JOH>
 A/Cross-references: GB:M29270; NID:g178863; PIDN:AAAS1768.1; PID:g178865
 R/Prelli, F.; Levy, E.; van Duinen, S.G.; Bots, G.T.A.M.; Luyendijk, W.;
 Frangione, B.
 Biochem. Biophys. Res. Commun. 170, 301-307, 1990
 A/Title: Expression of a normal and variant Alzheimer's beta-protein gene in
 amyloid of hereditary cerebral hemorrhage, Dutch type: DNA and protein
 diagnostic assays.
 A/Reference number: A35486; MJID:90321244; PMID:2196878
 A/Accession: A35486
 A/Molecule type: DNA
 A/Residues: 672-710 <PRE1>
 A/Note: 693-Gln was found in DNA isolated from HCMA-D patients
 R/Yoshikai, S.I.; Sasaki, H.; Don-ura, K.; Furuya, H.; Sakaki, Y.
 Gene 87, 257-263, 1990
 A/Title: Genomic organization of the human amyloid beta-protein precursor gene.
 A/Reference number: I39451; MJID:90236318; PMID:2110105
 A/Accession: I39452

A/Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-770 <YOS1>

A/Cross-references: GB:M3112; NID:gl78613; PIDN:AA59502.1; PID:gl78616

A/Accession: I39451

A/Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-530, QWLMFVPATWEAKVGR <YOS2>

A/Cross-references: GB:M34875; NID:gl78608; PIDN:AA59501.1; PID:gl78615

R/Yoshikawa, S.I.; Sasaki, H.; Doh-ure, K.; Furuue, H.; Sakaki, Y. Gene 102, 291-292, 1991

A/Reference number: A59020; MUID:91340168; PMID:1908403

A/Contents: annotation; erratum

A/Note: revised physical map for reference I39451

R/Levy, E.; Gorman, M.D.; Fernandez-Nadrid, I.J.; Power, M.D.; Lieberburg, I.; van Duinen, S.G.; Bots, G.T.; Luyendijk, W.; Frangione, B. Science 248, 1124-1126, 1990

A/Title: Mutation of the Alzheimer's disease amyloid gene in hereditary cerebral hemorrhage, Dutch type.

A/Reference number: I39453; MUID:90260663; PMID:2111584

A/Accession: I39453

A/Status: translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 636-737 <LEV>

A/Cross-references: GB:M37896; NID:gl78618; PIDN:AA51727.1; PID:gl78620

A/Note: a mutation with 693-Gln is presented

R/Murrell, J.; Farlow, M.; Ghetti, B.; Benson, M.D. Science 254, 97-99, 1991

A/Title: A mutation in the amyloid precursor protein associated with hereditary Alzheimer's disease.

A/Reference number: I59562; MUID:92022553; PMID:1925564

A/Accession: I59562

A/Status: translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 689-716, 'F', 718-737 <MUR>

A/Cross-references: GB:S57665; NID:q236720; PIDN:AA51991.1; PID:q236721

R/Kamino, K.; Orr, H.T.; Payami, H.; Williams, E.M.; Alonso, M.E.; Pulst, S.M.; Anderson, L.; O'Fall, S.; Nemens, E.; White, J.A.; Sadowick, A.D.; Ball, M.J.; Kaye, J.; Warren, A.; McInnis, M.; Antonarakis, S.E.; Korenberg, J.R.; Sharma, V.; Kukull, W.; Larson, E.; Heston, L.L.; Martin, G.M.; Bird, T.D.; Schellenberg, G.D. Am. J. Hum. Genet. 51, 998-1014, 1992

A/Title: Linkage and mutational analysis of familial Alzheimer disease kindreds for the APP gene region.

A/Reference number: A44017; MUID:93035397; PMID:1415269

A/Accession: A44017

A/Molecule type: DNA

A/Residues: 687-692, 'G', 694-718 <KAM1>

A/Cross-references: GB:S45135; NID:q257377; PIDN:AA523645.1; PID:q257378

A/Experimental source: familial Alzheimer disease family 58

A/Note: sequence extracted from NCBI backbone (NCBIP:115374)

A/Accession: B44017

A/Molecule type: DNA

A/Residues: 687-718 <KAM2>

A/Cross-references: GB:S45136; NID:q257379; PIDN:AA523646.1; PID:q257380

A/Experimental source: familial Alzheimer disease family LIT

A/Note: sequence extracted from NCBI backbone (NCBIP:115376)

A/Note: this sequence has a silent mutation

R/Kang, J.; Lemaire, H.G.; Unterbeck, A.; Salbaum, J.M.; Masters, C.L.; Grzeschik, K.H.; Multhaup, G.; Beyreuther, K.; Muller-Hill, B. Nature 335, 733-736, 1987

A/Title: The precursor of Alzheimer's disease amyloid A4 protein resembles a cell-surface receptor.

A/Reference number: A03134; MUID:87144572; PMID:2881207

A/Accession: A03134

A/Molecule type: mRNA

A/Residues: 1-288, 'V', 365-770 <KAN>

A/Cross-references: GB:Y00264; NID:q28525; PIDN:CAA68374.1; PID:q28526

A/Note: alternative splice form AP(695)

R/Robakis, N.K.; Ramakrishna, N.; Wolfe, G.; Wisniewski, H.M. Proc. Natl. Acad. Sci. U.S.A. 84, 4190-4194, 1987

A/Title: Molecular cloning and characterization of a cDNA encoding the cerebrovascular and the neuritic plaque amyloid peptides.

A/Reference number: A29030; MUID:87231971; PMID:3035574

A/Accession: A29030

A/Molecule type: mRNA

A/Residues: 284-288, 'V', 365-646, 'E', 648-770 <ROB>

A/Cross-references: GB:M16785; NID:gl78539; PIDN:AAA51722.1; PID:gl78540

A/Note: the authors translated the codon GAG for residue 647 as Asp

R/Goldgaber, D.; Lerman, M.I.; McBride, O.W.; Saffioti, U.; Gajdusek, D.C. Science 235, 877-880, 1987

A/Title: Characterization and chromosomal localization of a cDNA encoding brain amyloid of Alzheimer's disease.

A/Reference number: A47584; MUID:87120328; PMID:3810169

A/Accession: A47584

A/Molecule type: mRNA

A/Residues: 674-756, 'S', 758-770 <GOL>

A/Cross-references: GB:M15533; NID:gl78706; PIDN:AAA35540.1; PID:gl78707

A/Experimental source: brain

R/Rianzi, R.E.; Gusella, J.F.; Watkins, P.C.; Bruns, G.A.P.; St George-Hyslop, P.; Van Keuren, M.L.; Patterson, D.; Fagan, S.; Kurnit, D.M.; Neve, R.L. Science 235, 880-884, 1987

A/Title: Amyloid beta protein gene: cDNA, mRNA distribution, and genetic linkage near the Alzheimer locus.

A/Reference number: A47585; MUID:87120329; PMID:2949367

A/Accession: A47585

A/Molecule type: mRNA

A/Residues: 674-703 <TAH1>

A/Cross-references: GB:M15532; NID:gl77957; PIDN:AAA51564.1; PID:gl77958

R/Dyck, T.; Weidemann, A.; Multhaup, G.; Salbaum, J.M.; Lemaire, H.G.; Kang, J.; Mueller-Hill, B.; Masters, C.L.; Beyreuther, K. EMBO J. 7, 949-957, 1988

A/Title: Identification, transmembrane orientation and biogenesis of the amyloid A4 precursor of Alzheimer's disease.

A/Reference number: S02638; MUID:88296437; PMID:2900137

A/Accession: S02638

A/Molecule type: mRNA

A/Residues: 672-678 <DYR>

R/Tanzi, R.E.; McClatchey, A.I.; Lamperti, E.D.; Villa-Komaroff, L.; Gusella, J.F.; Neve, R.L. Nature 331, 528-530, 1988

A:/title: Protease inhibitor domain encoded by an amyloid protein precursor mRNA associated with Alzheimer's disease.
 A:/reference number: S00707; MUID:88122640; PMID:2893290.
 A:/accession: S00707
 A:/molecule type: mRNA
 A:/residues: 286-344, 'I', 365-366 <TAN2>
 A:/cross-references: EMBL:X06982; NID:g28817; PIDN:CAA30042.1; PID:g929612
 A:/experimental source: promyelocytic leukemia cell line HL60
 A:/note: alternative splice form APP(751)
 R:/Fonte, P.; Gonzalez-Dawhitt, P.; Schilling, J.; Miller, J.; Hsu, D.; Greenberg, B.; Davis, K.; Wallace, W.; Lieberburg, I.; Fuller, F.; Cordell, B. Nature 331, 525-527, 1988
 A:/title: A new A4 amyloid mRNA contains a domain homologous to serine proteinase inhibitors.
 A:/reference number: S00925; MUID:88122639; PMID:2893289
 A:/accession: S00925
 A:/molecule type: mRNA
 A:/residues: 1-344, 'I', 365-770 <P02>
 A:/cross-references: GB:X06989; EMBL:X00297; NID:g28720; PIDN:CAA30050.1; PID:g28721
 A:/note: alternative splice form APP(751)
 R:/Kitaguchi, N.; Takahashi, Y.; Tokushima, Y.; Shiojiri, S.; Ito, H. Nature 331, 530-532, 1988
 A:/title: Novel precursor of Alzheimer's disease amyloid protein shows protease inhibitory activity.
 A:/reference number: A38949; MUID:88122641; PMID:2893291
 A:/accession: A38949
 A:/molecule type: mRNA
 A:/residues: 287-367 <KIT>
 A:/cross-references: GB:X06981; NID:g28816; PIDN:CAA30041.1; PID:g929611
 A:/experimental source: glioblastoma cell line
 A:/note: alternative splice form APP(770)
 R:/Vitek, M.P.; Rasool, C.G.; de Sauvage, F.; Vitek, S.M.; Bartus, R.T.; Beer, B.; Ashton, R.A.; Macq, A.F.; Maloteaux, J.M.; Blume, A.J.; Octave, J.N. Brain Res. Mol. Brain Res. 4, 121-131, 1988
 A:/title: Absence of mutation in the beta-amyloid cDNAs cloned from the brains of three patients with sporadic Alzheimer's disease.
 A:/reference number: A30320
 A:/accession: A30320
 A:/status: not compared with conceptual translation
 A:/molecule type: mRNA
 A:/residues: 284-288, 'V', 365-770 <VIT1>
 A:/accession: B30320
 A:/status: not compared with conceptual translation
 A:/molecule type: mRNA
 A:/residues: 122-288, 'V', 365-770 <VIT2>
 A:/accession: C30320
 A:/status: not compared with conceptual translation
 A:/molecule type: mRNA
 R:/Zain, S.B.; Salim, M.; Chou, W.G.; Sajdel-Sulkowska, E.M.; Majocha, R.E.; Marotta, C.A. Proc. Natl. Acad. Sci. U.S.A. 85, 929-933, 1988
 A:/title: Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer disease brain: coding and noncoding regions of the fetal precursor mRNA are expressed in the cortex.
 A:/reference number: A31087; MUID:88124954; PMID:2893379

A:/accession: A31087
 A:/molecule type: mRNA
 A:/residues: 507-770 <ZAI>
 A:/cross-references: GB:M18734; NID:g178572; PIDN:AAA51726.1; PID:g178573
 A:/note: the authors translated the codon GAA for residue 599 as Gly, ACC for residue 603 as Val, GTG for residue 604 as Glu, GAG for residue 605 as Leu, CTT for residue 607 as Pro, CCC for residue 608 as Val, GTG for residue 609 as Asn, AAT for residue 610 as Gly, and GGT for residue 635 as Ser
 A:/note: the cited Genbank accession number, J03594, is not in release 101.0
 R:/Masters, C.L.; Multhaup, G.; Simms, G.; Pottgiesser, J.; Martins, R.N.; Beyreuther, K. Query Match 100.0%; Score 52; DB 1; Length 770;
 Best Local Similarity 100.0%; Pred. No. 0.055;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KQYTSIHG 9
 Db 726 KQYTSIHG 734
 Search completed: October 4, 2004, 18:58:23
 Job time : 20.3043 secs

OM protein - protein search, using sw model

Run on: October 4, 2004, 18:44:39 ; Search time 7.43478 Seconds
(without alignments)
63.032 Million cell updates/sec

Title: US-10-048-203-2

Perfect score: 52

Sequence: 1 KQYTSIHG 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	52	100.0	737	1 A4_FUGRU	Q93279 fugu rubrip
2	52	100.0	751	1 A4_SAISC	Q92441 s amyloid b
3	52	100.0	770	1 A4_CAVPO	Q60495 c amyloid b
4	52	100.0	770	1 A4_HUMAN	P05067 h amyloid b
5	52	100.0	770	1 A4_MACFA	P53601 m amyloid b
6	52	100.0	770	1 A4_MOUSE	P12023 m amyloid b
7	52	100.0	770	1 A4_PIG	P79307 r amyloid b
8	52	100.0	770	1 A4_RAT	P08592 r amyloid b
9	52	100.0	780	1 A4_TETFL	Q73683 tetraodon f
10	39	75.0	452	1 NU4M_LUMTE	Q34949 lumbricus t
11	38	73.1	488	1 YGM9_YEAST	Q01163 saccharomyc
12	35	67.3	197	1 PSD9_CAEEL	Q10920 caenorhabdi
13	35	67.3	443	1 GAT3_HUMAN	P23771 homo sapien
14	35	67.3	443	1 GAT3_MOUSE	P23772 mus musculu
15	35	67.3	739	1 PURL_LISIN	Q92an9 listeria in
16	35	67.3	739	1 PURL_LISMO	Q8yec1 listeria mo
17	35	67.3	1268	1 YRD6_CAEEL	Q09575 caenorhabdi

18	34	65.4	1406	1 TOP1_CANGA	O93794 candida gla
19	33	63.5	117	1 HEMU_LINUN	P22765 lingula ung
20	33	63.5	142	1 Y4KO_RHLSN	P55535 rhizobium s
21	33	63.5	157	1 SSRP_CHUTE	Q8Kw48 chlorobium
22	33	63.5	339	1 RF3A_XENBO	P17342 xenopus bor
23	33	63.5	361	1 SERC_BACHD	Q9Kdm4 bacillus ha
24	33	63.5	366	1 TF3A_XENLA	P03001 xenopus lae
25	33	63.5	379	1 ISPH_SYNY3	Q55643 synechocyst
26	33	63.5	519	1 LEU1_CANBF	Q7Vdj6 candidatus
27	33	63.5	530	1 UDBE_RAT	P36511 rattus norv
28	33	63.5	530	1 UDBE_RABIT	P36513 oryctolagus
29	33	63.5	645	1 ACS2_PSEAE	Q9Hv66 pseudomonas
30	33	63.5	683	1 CV19_HUMAN	Q13769 homo sapien
31	33	63.5	805	1 DF19_CAEEL	Q09555 caenorhabdi
32	33	63.5	4344	1 DYHC_ENEMI	P45444 emericella
33	32	61.5	121	1 OMF7_STAUA	P21223 staphylococ
34	32	61.5	239	1 DCUR_ECOLI	P59338 escherichia
35	32	61.5	239	1 DCUR_SHIEL	P39271 escherichia
36	32	61.5	239	1 DCUR_SHIEL	P59339 shigella fl
37	32	61.5	249	1 CREB_CHLVR	P51984 chlorohydra
38	32	61.5	284	1 YMK7_YEAST	Q04299 saccharomyc
39	32	61.5	326	1 ZN73_HUMAN	O43830 homo sapien
40	32	61.5	340	1 LFXD_WIGBR	Q6d2h2 wigglewort
41	32	61.5	352	1 GBAL_COPCO	P30675 coprinus co
42	32	61.5	510	1 CP12_DROME	P20385 drosophila
43	32	61.5	579	1 YCL2_KLEPN	Q48458 klebsiella
44	32	61.5	580	1 SYD_MYCPE	Q8wb67 mycoplasma
45	32	61.5	717	1 YCC5_ECOLI	P75870 escherichia

ALIGNMENTS

RESULT 1

A4_FUGRU	ID	A4_FUGRU	STANDARD	PRT	737 AA
AC	O93279;				
DT	10-OCT-2003 (Rel. 42, Created)				
DT	10-OCT-2003 (Rel. 42, Last sequence update)				
DT	10-OCT-2003 (Rel. 42, Last annotation update)				
DE	Alzheimer's disease amyloid A4 protein homolog precursor [Contains: Beta-amyloid protein (Beta-APP) (A-beta)].				
GN	APP.				
OS	Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;				
OC	Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;				
OC	Tetraodontidae; Tetraodontidae; Takifugu.				
OX	NCBI_TaxID=31033;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=98252138; PubMed=9599080;				
RA	Villard L., Tassone F., Cnengorac-Jurcevic T., Clancy K., Gardiner K.;				
RT	"Analysis of pufferfish homologues of the AT-rich human APP gene.";				
RL	Gene 210:17-24(1998).				
CC	-!- FUNCTION: Functional neuronal receptor which couples to intracellular signaling pathway through the G1P-binding protein .				

CC G10) (By similarity).

CC -|- SUBCELLULAR LOCATION: Type I membrane protein.

CC -|- SIMILARITY: Belongs to the APP family.

CC -|- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.

CC -----

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CC -----

CC EMBL; AF090120; AAD13392.1; -.

CC HSSP; P05067; 1HZ3.

CC InterPro; IPR008155; A4_APP.

CC InterPro; IPR008154; A4_extra.

CC InterPro; IPR001255; Beta-APP.

CC InterPro; IPR002223; Kunitz_BPTI.

CC Pfam; PF02177; A4_EXTRA; 1.

CC Pfam; PF03494; Beta-APP; 1.

CC Pfam; PF00014; Kunitz_BPTI; 1.

CC PRINTS; PR00203; AMYLOIDA4.

CC PRINTS; PR00759; BASICPTASE.

CC ProDom; PD000222; Kunitz_BPTI; 1.

CC SMART; SM00006; A4_EXTRA; 1.

CC SMART; SM00131; K01; 1.

CC PROSITE; PS00319; A4_EXTRA; FALSE_NEG.

CC PROSITE; PS00320; A4_INTRA; 1.

CC PROSITE; PS00280; BPTI_KUNITZ_1; 1.

CC PROSITE; PS00279; BPTI_KUNITZ_2; 1.

CC Glycoprotein; Amyloid; Neurone; Transmembrane; Signal;

CC Serine protease inhibitor.

FT SIGNAL 1 18 POTENTIAL.

FT CHAIN 19 737 ALZHEIMER'S DISEASE AMYLOID A4

FT CHAIN 639 681 PROTEIN HOMOLOG.

FT DOMAIN 19 668 BETA-AMYLOID PROTEIN (POTENTIAL).

FT TRANSMEM 669 689 EXTRACELLULAR (POTENTIAL).

FT DOMAIN 690 737 POTENTIAL.

FT DOMAIN 286 344 CYTOPLASMIC (POTENTIAL).

FT SITE 726 729 BPTI/KUNITZ INHIBITOR.

FT ACT_SITE 300 301 CLATHRIN-BINDING (BY SIMILARITY).

FT DISULFID 290 340 REACTIVE BOND.

FT DISULFID 299 323 BY SIMILARITY.

FT DISULFID 315 336 BY SIMILARITY.

FT CARBOHYD 522 522 N-LINKED (GLCNAC...) (POTENTIAL).

SQ SEQUENCE 737 AA; 82856 MW; 6FAD01E2E3B2B7E2 CRC64;

Query Match 100.0% Score 52; DS 1; Length 737;

Best Local Similarity 100.0%; Pred. No. 0.016;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KQYTSIHHG 9

Db 693 KQYTSIHHG 701

RESULT 2

A4_SAISC

ID A4_SAISC STANDARD; PRT; 751 AA.

AC Q95241;

DT 15-DEC-1998 (Rel. 37, Created)

DT 15-DEC-1998 (Rel. 37, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Amyloid beta A4 protein precursor (APP) (Alzheimer's disease amyloid

DE protein homolog) [Contains: Soluble APP-alpha (S-APP-alpha); Soluble

DE APP-beta (S-APP-beta); C99; Beta-amyloid protein 42 (Beta-APP42);

DE Beta-amyloid protein 40 (Beta-APP40); C83; P3(42); P3(40); Gamma-

DE CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-CTF(57)

DE (Gamma-secretase C-terminal fragment 57); Gamma-CTF(50) (Gamma-

DE secretase C-terminal fragment 50); C31].

GN APP.

OS Saimiri sciureus (Common squirrel monkey).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae; Saimiri.

OX NCBI_TaxID=9521;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Kidney, and Liver;

RX MEDLINE=96108492; PubMed=8532114;

RA Levy E., Amorn A., Frangione B., Walker L.C.;

RT "Beta-amyloid precursor protein gene in squirrel monkeys with

RT cerebral amyloid angiopathy."

RL Neurobiol. Aging 16:805-808(1995).

CC -|- FUNCTION: Functions as a cell surface receptor and performs

CC physiological functions on the surface of neurons relevant to

CC neurite growth, neuronal adhesion and axonogenesis. Involved in

CC cell mobility and transcription regulation through protein-protein

CC interactions (By similarity). Can promote transcription activation

CC through binding to APBB1/Tip60 and inhibit Notch signaling through

CC interaction with Numb (By similarity). Couples to apoptosis-

CC inducing pathways such as those mediated by G(O) and JIP (By

CC similarity). Inhibits G(O) alpha Appase activity (By similarity).

CC Acts as a kinesin I membrane receptor, mediating the axonal

CC transport of beta-secretase and presenilin 1 (By similarity). May

CC be involved in copper homeostasis/oxidative stress through copper

CC ion reduction. In vitro, copper-metallated APP induces neuronal

CC death directly or is potentiated through Cu(II)-mediated low-

CC density lipoprotein oxidation (By similarity). Can regulate

CC neurite outgrowth through binding to components of the

CC extracellular matrix such as heparin and collagen I and IV (By

CC similarity). The splice isoforms that contain the BPTI domain

CC possess protease inhibitor activity (By similarity).

CC -|- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators

CC with metal-reducing activity. Bind transient metals such as

CC copper, zinc and iron (By similarity).

CC -|- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved

CC peptides, including C31, are potent enhancers of neuronal

CC apoptosis (By similarity).

CC -|- SUBUNIT: Binds, via its C-terminal, to the PID domain of several

CC cytoplasmic proteins, including APBB family members, the APBA

CC family, MAPK8IP1, and SHC1, Numb and Dab1 (By similarity). Binding

CC to Dab1 inhibits its serine phosphorylation (By similarity). Also

interacts with GPCR-like protein BPE, FPL1, APPBP1, IBL, KNS2 (via its TPR domain) (By similarity). APPBP2 (via BASS) and DDB1. In vitro, it binds WAPF via the WT-binding domains (By similarity). Associates with microtubules in the presence of ATP and in a kinesin-dependent manner (By similarity).

-| SUBCELLULAR LOCATION: Type I membrane protein. Cell surface protein that rapidly becomes internalized via clathrin-coated pits. During maturation, the immature APP (N-glycosylated in the endoplasmic reticulum) moves to the Golgi complex where complete maturation occurs (O-glycosylated and sulfated). After alpha-secretase cleavage, soluble APP is released into the extracellular space and the C-terminal is internalized to endosomes and lysosomes. Some APP accumulates in secretory transport vesicles leaving the late Golgi compartment and returns to the cell surface. Gamma-Ctf(59) peptide is located to both the cytoplasm and nuclei of neurons (By similarity).

-| ALTERNATIVE PRODUCTS:

Event=Alternative splicing; Named isoforms=2;
Comment=Additional isoforms seem to exist;
Name=APP770;
Name=APP695;
IsoId=Q95241-1; Sequence=Displayed;
IsoId=Q95241-2; Sequence=Not described;

-| DOMAIN: The basolateral sorting signal (BASS) is required for sorting of membrane proteins to the basolateral surface of epithelial cells (By similarity).

-| DOMAIN: The NPXY sequence motif found in many tyrosine-phosphorylated proteins is required for the specific binding of the PID domain. However additional amino acids either N- or C-terminal to the NPXY motif are often required for complete interaction. The PID domain-containing proteins which bind APP require the YENPTY motif for full interaction. These interactions are independent of phosphorylation on the terminal tyrosine residue. The NPXY site is also involved in clathrin-mediated endocytosis (By similarity).

-| PTM: Proteolytically processed under normal cellular conditions. Cleavage by alpha-secretase or alternatively by beta-secretase leads to generation and extracellular release of soluble APP peptides, S-APP-alpha and S-APP-beta, respectively, and the retention of corresponding membrane-anchored C-terminal fragments, C83 and C99. Subsequent processing of C83 by gamma-secretase yields P3 peptides. This is the major secretory pathway and is nonamyloidogenic. Alternatively, presenilin/nicastrin-mediated gamma-secretase processing of C99 releases the amyloid beta proteins, amyloid-beta 40 (Abeta40) and amyloid-beta 42 (Abeta42), major components of amyloid plaques, and the cytotoxic C-terminal fragments, gamma-CTF(50), gamma-CTF(57) and gamma-CTF(59) (By similarity).

-| PTM: Proteolytically cleaved by caspases during neuronal apoptosis (By similarity). Cleavage at Asp-720 by either caspase-3, -8 or -9 results in the production of the neurotoxic C31 peptide and the increased production of beta-amyloid peptides (By similarity).

-| PTM: N- and O-glycosylated (By similarity).

-| PTM: Phosphorylation in the C-terminal on tyrosine, threonine and serine residues is neuron-specific. Phosphorylation can affect APP processing, neuronal differentiation and interaction with other proteins (By similarity).

-| MISCELLANEOUS: Chelation of metal ions, notably copper, iron and zinc, can induce histidine-bridging between beta-amyloid molecules resulting in beta-amyloid-metal aggregates (By similarity). Extracellular zinc-binding increases binding of heparin to APP and inhibits collagen-binding (By similarity).

-| SIMILARITY: Belongs to the APP family.

-| SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.

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EMBL: S81024; AADI4347.1; -
HSSP: P05067; IAPP
InterPro: IPR008155; A4_APP.
InterPro: IPR008154; A4_extra.
InterPro: IPR001255; Beta-APP.
InterPro: IPR002223; Kunitz_BPTI.
Pfam: PF02177; A4_EXTRA; 1.
Pfam: PF03494; Beta-APP; 1.
Pfam: PF00014; Kunitz_BPTI; 1.
PRINTS: PR00203; AMYLOIDA4.
PRINTS: PR00739; BASICPTASE.

ProDom: PD000222; Kunitz_BPTI; 1.
SMART: SMO0006; A4_EXTRA; 1.
SMART: SMO0131; KU; 1.
PROSITE: PS00319; A4_EXTRA; 1.
PROSITE: PS00320; A4_INTRA; 1.
PROSITE: PS00280; BPTI_KUNITZ_1; 1.
PROSITE: PS00279; BPTI_KUNITZ_2; 1.
Apoptosis; Endocytosis; Cell adhesion; Serine protease inhibitor; Coated pits; Neurone; Heparin-binding; Metal-binding; Copper; Iron; Zinc; Signal; Transmembrane; Glycoprotein; Phosphorylation; Proteoglycan; Amyloid; Alternative splicing.
FT SIGNAL 1 17 BY SIMILARITY.
FT CHAIN 18 731 A4 PROTEIN.
FT CHAIN 18 668 SOLUBLE APP-ALPHA (POTENTIAL).
FT CHAIN 18 652 SOLUBLE APP-BETA (POTENTIAL).
FT CHAIN 653 751 C99 (POTENTIAL).
FT CHAIN 653 694 BETA-AMYLOID PROTEIN 42 (POTENTIAL).
FT CHAIN 653 692 BETA-AMYLOID PROTEIN 40 (POTENTIAL).
FT CHAIN 669 751 C83 (POTENTIAL).
FT CHAIN 669 692 P3(42) (POTENTIAL).
FT CHAIN 669 692 P3(40) (POTENTIAL).
FT CHAIN 693 751 GAMMA-CTF(59) (POTENTIAL).
FT CHAIN 695 751 GAMMA-CTF(57) (POTENTIAL).
FT CHAIN 702 751 GAMMA-CTF(50) (POTENTIAL).
FT CHAIN 721 751 C31 (POTENTIAL).
FT DOMAIN 18 680 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 681 704 POTENTIAL.
FT DOMAIN 705 751 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 96 110 HEPARIN-BINDING (BY SIMILARITY).

FT DOMAIN 181 188 ZINC-BINDING (BY SIMILARITY).
 FT DOMAIN 291 341 BPTI/KUNITZ INHIBITOR.
 FT DOMAIN 316 344 HEPARIN-BINDING (BY SIMILARITY).
 FT DOMAIN 363 428 HEPARIN-BINDING (BY SIMILARITY).
 FT DOMAIN 504 521 COLLAGEN-BINDING (BY SIMILARITY).
 FT DOMAIN 713 732 INTERACTION WITH G(O)-ALPHA
 (BY SIMILARITY).
 FT DOMAIN 230 260 ASP/GLU-RICH (ACIDIC).
 FT DOMAIN 274 280 POLY-THR.
 FT SITE 144 144 REQUIRED FOR COPPER(II) REDUCTION
 (BY SIMILARITY).
 FT ACT_SITE 301 302 REACTIVE BOND.
 FT SITE 652 653 CLEAVAGE (BY BETA-SECRETASE)
 (BY SIMILARITY).
 FT SITE 653 654 CLEAVAGE (BY CASPASE-6) (BY SIMILARITY).
 FT SITE 668 669 CLEAVAGE (BY ALPHA-SECRETASE)
 (BY SIMILARITY).
 FT SITE 685 685 INVOLVED IN FREE RADICAL PROPAGATION
 (BY SIMILARITY).
 FT SITE 687 687 INVOLVED IN OXIDATIVE REACTIONS
 (BY SIMILARITY).
 FT SITE 692 693 CLEAVAGE (BY GAMMA-SECRETASE; SITE 1)
 (BY SIMILARITY).
 FT SITE 694 695 CLEAVAGE (BY GAMMA-SECRETASE; SITE 2)
 (BY SIMILARITY).
 FT SITE 701 702 CLEAVAGE (BY GAMMA-SECRETASE; SITE 3)
 (BY SIMILARITY).
 FT SITE 705 715 BASOLATERAL SORTING SIGNAL
 (BY SIMILARITY).
 FT SITE 720 721 CLEAVAGE (BY CASPASES-3,-6,-8 OR -9)
 (BY SIMILARITY).
 FT SITE 738 741 ENDOCYTOSIS SIGNAL.
 FT SITE 740 743 NPXY MOTIF.

Query Match 100.0%; Score 52; DB 1; Length 751;
 Best Local Similarity 100.0%; Pred. No. 0.016;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KQYTSIHG 9
 |||||
 Db 707 KQYTSIHG 715

RESULT 3
 A4_CAVPO
 AC A60495; Q60496; PRT; 770 AA.
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DE Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
 amyloid protein homolog) [Contains: Soluble APP-alpha (S-APP-alpha);
 Soluble APP-beta (S-APP-beta); CTF-alpha; CTF-beta; Beta-amyloid
 protein 42 (Beta-APP42); Beta-amyloid protein 40 (Beta-APP40); P3(42);
 P3(40); CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-
 APP.
 GN APP.

OS Cavia porcellus (Guinea pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
 CX NCBI_taxID=10141;
 RN [1]
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
 RC TISSUE=Brain, and Liver;
 RX MEDLINE=97236426; PubMed=9116031;
 RA Beck M., Mueller D., Bigl V.;
 RT "Amyloid precursor protein in Guinea pigs - complete cDNA sequence and
 alternative splicing."; Biochem. Biophys. Acta 1351:17-21(1997).
 RL [2]
 RN [2]
 RP INTERACTION OF BETA-APP40 WITH APOE.
 RX MEDLINE=98007700; PubMed=9349544;
 RA Martel C.L., MacKie J.B., Mattsbara E., Governale S., Miguel C.,
 Miao W., McComb J.G., Frangione B., Ghiso J., Zlokovic B.V.;
 RT "Isoform-specific effects of apolipoproteins E2, E3, and E4 on
 cerebral capillary sequestration and blood-brain barrier transport of
 circulating Alzheimer's amyloid beta."; J. Neurochem. 69:1995-2004(1997).
 RL [3]
 RN [3]
 RP PROCESSING.
 RX MEDLINE=20084499; PubMed=10619481;
 RA Beck M., Bruckner M.K., Holzer M., Kaap S., Pannicke T., Arendt T.,
 Bigl V.;
 RT "Guinea-pig primary cell cultures provide a model to study expression
 and amyloidogenic processing of endogenous amyloid precursor
 protein."; J. Biol. Chem. 276:481-487(2001).
 RL [4]
 RN [4]
 RP GAMMA-SECRETASE PROCESSING.
 RX MEDLINE=20576391; PubMed=11035007;
 RA Pinnix I., Musunuru U., Tun H., Sridharan A., Golde T., Eckman C.,
 Ziani-Cherif C., Onstead L., Sambamurti K.;
 RT "A novel gamma -secretase assay based on detection of the putative
 C-terminal fragment-gamma of amyloid beta protein precursor."; J. Biol. Chem. 276:481-487(2001).
 CC -|- FUNCTION: Functions as a cell surface receptor and performs
 physiological functions on the surface of neurons relevant to
 neurite growth, neuronal adhesion and axonogenesis. Involved in
 cell mobility and transcription regulation through protein-protein
 interactions (By similarity). Can promote transcription activation
 through binding to APBB1/Tip60 and inhibit Notch signaling through
 interaction with Numb (By similarity). Couples to apoptosis-
 inducing pathways such as those mediated by G(O) and JIP (By
 similarity). Inhibits G(O) alpha ATPase activity (By similarity).
 Acts as a kinesin I membrane receptor, mediating the axonal
 transport of beta-secretase and presenilin 1 (By similarity). May
 be involved in copper homeostasis/oxidative stress through copper
 ion reduction (By similarity). In vitro, copper-metallated APP
 induces neuronal death directly or is potentiated through Cu(II)-
 mediated low-density lipoprotein oxidation (By similarity). Can
 regulate neurite outgrowth through binding to components of the
 extracellular matrix such as heparin and collagen I and IV (By
 similarity). The splice isoforms that contain the BPTI domain
 possess protease inhibitor activity (By similarity).

-| FUNCTION: Beta-amyloid peptides are lipophilic metal chelators with metal-reducing activity. Bind transient metals such as copper, zinc and iron. Beta-amyloid peptides bind to lipoproteins and apolipoproteins E and J in the CSF and to HDL particles in plasma, inhibiting metal-catalyzed oxidation of lipoproteins.

-| FUNCTION: Apolipins elicit adhesion of neural cells to the extracellular matrix and may regulate neurite outgrowth in the brain (By similarity).

-| FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved peptides, including C31, are potent enhancers of neuronal apoptosis (By similarity).

-| SUBUNIT: Binds, via its C-terminal, to the PID domain of several cytoplasmic proteins, including APBB family members, the APBA family, MAPK6IP1, SHC1 and Numb and Dab1 (By similarity). Also interacts with GPCR-like protein BPP, FPR1L1, APPBP1, IBI1, KNS2 (via its TPR domains), APPBP2 (via BASS) and DBI1 (By similarity). Associates with microtubules in the presence of ATP and in a kinesin-dependent manner (By similarity). Soluble Abeta40 binds all three isoforms of APOB, in vitro and in vivo. When lipidated, APOB3 appears to be the preferred amyloid binding isoform, while the apoB4 isoform-beta-APP40 complex is capable of being transported across the blood-brain barrier.

-| SUBCELLULAR LOCATION: Type I membrane protein. Cell surface protein that rapidly becomes internalized via clathrin-coated pits (By similarity). During maturation, the immature APP (N-glycosylated in the endoplasmic reticulum) moves to the Golgi complex where complete maturation occurs (O-glycosylated and suited) (By similarity). After alpha-secretase cleavage, soluble APP is released into the extracellular space and the C-terminal is internalized to endosomes and lysosomes (By similarity). Some APP accumulates in secretory transport vesicles leaving the late Golgi compartment and returns to the cell surface (By similarity). APP sorts to the basolateral surface in epithelial cells (By similarity).

-| ALTERNATIVE PRODUCTS:

Event=Alternative splicing; Named isoforms=2;
Comment=Additional isoforms, missing exons 7,8 and 15, seem to exist. The L-isoforms, missing exon 15, are referred to as apolipins;
Name=APP770;
IsoId=Q60495-1; Sequence=Displayed;
Name=APP695;
IsoId=Q60495-2; Sequence=VSP_007221, VSP_007222;

-| TISSUE SPECIFICITY: Isoform APP695 is the major isoform found in brain. The longer isoforms containing the EPTI domain are predominantly expressed in peripheral organs such as muscle and liver.

-| INDUCTION: Increased levels during neuronal differentiation.

-| DOMAIN: The basolateral sorting signal (BASS) is required for sorting of membrane proteins to the basolateral surface of epithelial cells.

-| DOMAIN: The NPXY sequence motif found in many tyrosine-phosphorylated proteins is required for the specific binding of the PID domain. However additional amino acids either N- or C-terminal to the NPXY motif are often required for complete interaction. The PID domain-containing proteins which bind APP require the YENPTY motif for full interaction. These interactions

DR PROSITE; P550279; BPTI_KUNITZ_2; 1.
 KW Apoptosis; Endocytosis; Cell adhesion; Serine protease inhibitor;
 KW Coated pits; Neurone; Heparin-binding; Metal-binding; Copper; Iron;
 KW Zinc; Signal; Transmembrane; Glycoprotein; Phosphorylation;
 KW Proteoglycan; Alternative splicing; Amyloid.
 FT SIGNAL 1 17
 FT CHAIN 18 770
 FT CHAIN 18 677
 FT CHAIN 18 671
 FT CHAIN 672 770
 FT CHAIN 672 713
 FT CHAIN 672 711
 FT CHAIN 688 770
 FT CHAIN 688 713
 FT CHAIN 688 711
 FT CHAIN 712 770
 FT CHAIN 714 770

Query Match 100.0%; Score 52; DB 1; Length 770;
 Best Local Similarity 100.0%; Pred. No. 0.017;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KQYTSIHG 9
 |||||
 Db 726 KQYTSIHG 734

RESULT 4
 A4_HUMAN STANDARD; PRT; 770 AA.
 AC P03067; P03000; P78438; Q13764; Q13778; Q13793; Q16011; Q16014;
 AC Q16019; Q16020; Q9ET38; Q9UCA9; Q9UCB6; Q9UCB8; Q9UCD1; Q9UC58;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 01-NOV-1991 (Rel. 20, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
 DE amyloid protein) (Cerebral vascular amyloid peptide) (CvAP) (Protease
 DE nexin-II) (PN-II) (APPI) (PreA4) (Contains: Soluble APP-alpha (S-APP-
 DE alpha); Soluble APP-beta (S-APP-beta); C99; Beta-amyloid protein 42
 DE (Beta-APP42); Beta-amyloid protein 40 (Beta-APP40); C83; P3(42);
 DE P3(40); Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59)
 DE (Amyloid intracellular domain 59) (AID(59)); Gamma-CTF(57) (Gamma-
 DE secretase C-terminal fragment 57) (Amyloid intracellular domain 57)
 DE (AID(57)); Gamma-CTF(50) (Gamma-secretase C-terminal fragment 50)
 DE (Amyloid intracellular domain 50) (AID(50)); C31).
 GN APP OR A4 OR AD1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM APP695).
 RC TISSUE=Brain;
 RX MEDLINE=67144572; PubMed=2881207;
 RA Kang J., Lemaire H.-G., Unterbeck A., Salbaum J.M., Masters C.L.,
 RA Grzeschik K.-H., Multhaup G., Beyreuther K., Mueller-Hill B.;
 RT "The precursor of Alzheimer's disease amyloid A4 protein resembles a

RT cell-surface receptor.";
 RL Nature 325:733-736(1997).
 [2]
 RP SEQUENCE FROM N.A. (ISOFORM APP751).
 RC TISSUE=Brain;
 RX MEDLINE=88122639; PubMed=2893289;
 RA Ponte P., Gonzalez-Dewhitt P., Schilling J., Miller J., Hau D.,
 RA Greenberg B., Davis K., Wallace W., Lieberburg I., Fuller F.,
 RA Cordell B.;
 RT "A new A4 amyloid mRNA contains a domain homologous to serine
 RT proteinase inhibitors.";
 RL Nature 331:525-527(1988).
 [3]
 RP SEQUENCE FROM N.A. (ISOFORM APP695).
 RX MEDLINE=89128427; PubMed=2783773;
 RA Lemaire H.-G., Salbaum J.M., Multhaup G., Kang J., Bayney R.M.,
 RA Unterbeck A., Beyreuther K., Mueller-Hill B.;
 RT "The PreA4(695) precursor protein of Alzheimer's disease A4 amyloid
 RT is encoded by 16 exons.";
 RL Nucleic Acids Res. 17:517-522(1989).
 [4]
 RP SEQUENCE FROM N.A. (ISOFORM APP770).
 RX MEDLINE=90236318; PubMed=2110105;
 RA Yoshikai S.-I., Sasaki H., Doh-Ura K., Furuya H., Sakaki Y.;
 RT "Genomic organization of the human amyloid beta-protein precursor
 RT gene.";
 RL Gene 87:257-263(1990).
 [5]
 RP ERRATUM, AND REVISIONS.
 RA Yoshikai S.-I., Sasaki H., Doh-ura K., Furuya H., Sakaki Y.;
 RL Gene 102:291-292(1991).
 [6]
 RP SEQUENCE FROM N.A. (ISOFORM L-APP733).
 RC TISSUE=Leukocyte;
 RX MEDLINE=92268136; PubMed=1587857;
 RA Koenig G., Moening U., Czech C., Prior R., Banati R.,
 RA Schreier-Gasser U., Bauer J., Masters C.L., Beyreuther K.;
 RT "Identification and differential expression of a novel alternative
 RT splice isoform of the beta A4 amyloid precursor protein (APP) mRNA in
 RT leukocytes and brain microglial cells.";
 RL J. Biol. Chem. 267:10804-10809(1992).
 [7]
 RP SEQUENCE FROM N.A. (ISOFORM APP770).
 RX MEDLINE=97263807; PubMed=9108164;
 RA Hattori M., Tsukihara F., Furuhata Y., Tanahashi H., Hirose M.,
 RA Saito M., Tsukuni S., Sakaki Y.;
 RT "A novel method for making nested deletions and its application for
 RT sequencing of a 300 kb region of human APP locus.";
 RL Nucleic Acids Res. 25:1802-1808(1997).
 [8]
 RP SEQUENCE FROM N.A. (ISOFORM APP639).
 RC TISSUE=Brain;
 RX MEDLINE=22744650; PubMed=12859342;
 RA Tang K., Wang C., Shen C., Sheng S., Ravid R., Jing N.;
 RT "Identification of a novel alternative splicing isoform of human
 RT amyloid precursor protein gene, APP639.";
 RL Eur. J. Neurosci. 18:102-108(2003).

RN SEQUENCE FROM N.A. (ISOFORM APP305).
 RP TISSUE=Pancreas;
 RX MEDLINE=2238257; PubMed=12477932;
 RA Strausberg R.L., Feilgold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant I.L., Scheetz T.E.,
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Frange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Wozley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kertman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16839-16903(2002).
 RN [10]
 RP SEQUENCE OF 1-10 FROM N.A.
 RP TISSUE=Liver;
 RX MEDLINE=89016647; PubMed=3140222;
 RA Schon E.A., Mita S., Sadlock J., Herbert J.;
 RT "A cDNA specifying the human amyloid beta precursor protein (ABPP)
 RT encodes a 95-kDa polypeptide.";
 RL Nucleic Acids Res. 16:9351-9351(1988).
 RN [11]
 RP ERRATUM, AND REVISIONS.
 RA Mita S., Sadlock J., Herbert J., Schon E.A.;
 RL Nucleic Acids Res. 16:11402-11402(1988).
 RN [12]
 RP SEQUENCE OF 1-75 FROM N.A.
 RX MEDLINE=89165870; PubMed=2538123;
 RA La Fauci G., Lahiri D.K., Salton S.R., Robakis N.K.;
 RT "Characterization of the 5'-end region and the first two exons of the
 RT beta-protein precursor gene.";
 RL Biochem. Biophys. Res. Commun. 159:297-304(1989).
 RN [13]
 RP SEQUENCE OF 18-50.
 RC TISSUE=Fibroblast;
 RX MEDLINE=87250462; PubMed=3597385;
 RA van Nostrand W.E., Cunningham D.D.;
 RT "Purification of protease nexin II from human fibroblasts.";
 RL J. Biol. Chem. 262:8508-8514(1987).
 RN [14]
 RP PARTIAL SEQUENCE FROM N.A. (ISOFORM APP751).
 RC TISSUE=Brain;
 RX MEDLINE=89346754; PubMed=2569763;
 RA de Sauvage F., Octave J.N.;
 RT "A novel mRNA of the A4 amyloid precursor gene coding for a possibly
 RT secreted protein."

RL Science 245:651-653(1989).
 RN [15]
 RP PARTIAL SEQUENCE FROM N.A. (ISOFORM APP695).
 RC TISSUE=Brain;
 RX MEDLINE=87231971; PubMed=3035574;
 RA Robakis N.K., Ramakrishna N., Wolfe G., Wisniewski H.M.;
 RT "Molecular cloning and characterization of a cDNA encoding the
 RT cerebrovascular and the neuritic plaque amyloid peptides.";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:4190-4194(1987).
 RN [16]
 RP SEQUENCE OF 286-366 FROM N.A.
 RX MEDLINE=88122640; PubMed=2893290;
 RA Tanzi R.E., McClatchey A.I., Lamperti E.D., Villa-Komaroff L.,
 RA Gusella J.F., Neve R.L.;
 RT "Protease inhibitor domain encoded by an amyloid protein precursor
 RT mRNA associated with Alzheimer's disease.";
 RL Nature 331:528-530(1988).
 RN [17]
 RP SEQUENCE OF 287-367 FROM N.A.
 RX MEDLINE=88122641; PubMed=2893291;
 RA Kitaguchi N., Takahashi Y., Tokushima Y., Shiojiri S., Ito H.;
 RT "Novel precursor of Alzheimer's disease amyloid protein shows
 RT protease inhibitory activity.";
 RL Nature 331:530-532(1988).
 RN [18]
 RP SEQUENCE OF 507-770 FROM N.A.
 RC TISSUE=Brain cortex;
 RX MEDLINE=88124954; PubMed=2893379;
 RA Zain S.B., Salim M., Chou W.G., Sajdel-Sulkowska E.M., Majocha R.E.,
 RA Marotta C.A.;
 RT "Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer
 RT disease brain: coding and noncoding regions of the fetal precursor
 RT mRNA are expressed in the cortex.";
 RL Proc. Natl. Acad. Sci. U.S.A. 85:929-933(1988).
 RN [19]
 RP SEQUENCE OF 523-555, AND COLLAGEN-BINDING DOMAIN.
 RX MEDLINE=96139497; PubMed=8576160;
 RA Behar D., Hesse L., Masters C.L., Multhaup G.;
 RT "Regulation of amyloid protein precursor (APP) binding to collagen and
 RT mapping of the binding sites on APP and collagen type I.";
 RL J. Biol. Chem. 271:1613-1620(1996).
 RN [20]
 RP SEQUENCE OF 655-737 FROM N.A., AND VARIANTS AD PHE-717; AD ILE-717
 AND AD GLY-717.
 RX MEDLINE=93236601; PubMed=8476439;
 RA Denman R.B., Rosenzweig R., Miller D.L.;
 RT "A system for studying the effect(s) of familial Alzheimer disease
 RT mutations on the processing of the beta-amyloid peptide precursor.";
 RL Biochem. Biophys. Res. Commun. 192:96-103(1993).
 RN [21]
 RP SEQUENCE OF 656-737 FROM N.A.
 RX MEDLINE=89392030; PubMed=2675837;
 RA Johnstone E.M., Chaney M.O., Moore R.E., Ward K.E., Norris F.H.,
 RA Little S.P.;
 RT "Alzheimer's disease amyloid peptide is encoded by two exons and shows
 RT similarity to soybean trypsin inhibitor.";
 RL Biochem. Biophys. Res. Commun. 163:1248-1255(1989).

RN [22]

Query Match 100.0%; Score 52; DB 1; Length 770;
Best Local Similarity 100.0%; Pzed. No. 0.017;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KQYTSIHG 9
|||||
Db 726 KQYTSIHG 734

RESULT 5

ID	A4 MACFA	STANDARD;	PRT;	770 AA.
AC	P53601; Q95XN7;			
DT	01-OCT-1996 (Rel. 34, Created)			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Amyloid beta A4 protein precursor (APP) (APP) (Alzheimer's disease amyloid protein homolog) (Contains: Soluble APP-alpha (S-APP-alpha); Soluble APP-beta (S-APP-beta); C99; Beta-amyloid protein 42 (Beta-APP42); Beta-amyloid protein 40 (Beta-APP40); C83; P3(42); P3(40); Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-CTF(57) (Gamma-secretase C-terminal fragment 57); Gamma-CTF(50) (Gamma-secretase C-terminal fragment 50); C31).			
GN	APP.			
OS	Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Cereopithecoidea; Macaca.			
OX	NCBI_TaxID=9541;			
RN	[1]			
RP	SEQUENCE FROM N.A. (ISOFORMS APP695 AND APP770).			
RC	TISSUE=Cerebellum;			
RX	MEDLINE=9127311; PubMed=1905108;			
RA	Podlinsky M.B., Tolan D.R., Selkoe D.J.;			
RT	"Homology of the amyloid beta protein precursor in monkey and human supports a primate model for beta amyloidosis in Alzheimer's disease.";			
RL	Am. J. Pathol. 138:1423-1435 (1991).			
CC	!- FUNCTION: Functions as a cell surface receptor and performs neurite growth, neuronal adhesion and axonogenesis. Involved in cell mobility and transcription regulation through protein-protein interactions (By similarity). Can promote transcription activation through binding to APBB1/Tip60 and inhibit Notch signaling through interaction with Numb (By similarity). Couples to apoptosis-inducing pathways such as those mediated by G(O) and JIP (By similarity). Inhibits G(O) alpha Affase activity (By similarity). Acts as a kinesin I membrane receptor, mediating the axonal transport of beta-secretase and presenilin 1 (By similarity). May be involved in copper homeostasis/oxidative stress through copper ion reduction. In vitro, copper-metallated APP induces neuronal death directly or is potentiated through Cu(II)-mediated low-density lipoprotein oxidation (By similarity). Can regulate neurite outgrowth through binding to components of the extracellular matrix such as heparin and collagen I and IV (By			

similarity). The splice isoforms that contain the BPTI domain possess protease inhibitor activity (By similarity).
!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators with metal-reducing activity. Bind transient metals such as copper, zinc and iron (By similarity).
!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved peptides, including C31, are potent enhancers of neuronal apoptosis (By similarity).
!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several cytoplasmic proteins, including APBB family members, the APBA family, MAPK8IP1, and SHC1, Numb and Dab1 (By similarity). Binding to Dab1 inhibits its serine phosphorylation (By similarity). Also interacts with GPCR-like protein BPP, F88L1, APPBP1, IBL1, KNS2 (via its TPR domains) (By similarity), APPBP2 (via BaSS) and DDB1. In vitro, it binds WAP1 via the W1-binding domains (By similarity). Associates with microtubules in the presence of ATP and in a kinesin-dependent manner (By similarity).
!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface protein that rapidly becomes internalized via clathrin-coated pits. During maturation, the immature APP (N-glycosylated in the endoplasmic reticulum) moves to the Golgi complex where complete maturation occurs (O-glycosylated and sulfated). After alpha-secretase cleavage, soluble APP is released into the extracellular space and the C-terminal is internalized to endosomes and lysosomes. Some APP accumulates in secretory transport vesicles leaving the late Golgi compartment and returns to the cell surface. Gamma-CTF(59) peptide is located to both the cytoplasm and nuclei of neurons (By similarity).
!- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;
Comment=Additional isoforms seem to exist;
Name=APP770;
IsoId=P53601-1; Sequence=Displayed;
Name=APP695;
IsoId=P53601-2; Sequence=VSP_000010, VSP_000011;
!- DOMAIN: The basolateral sorting signal (BaSS) is required for sorting of membrane proteins to the basolateral surface of epithelial cells (By similarity).
!- DOMAIN: The NPXY sequence motif found in many tyrosine-phosphorylated proteins is required for the specific binding of the PID domain. However additional amino acids either N- or C-terminal to the NPXY motif are often required for complete interaction. The PID domain-containing proteins which bind APP require the YENPTY motif for full interaction. These interactions are independent of phosphorylation on the terminal tyrosine residue. The NPXY site is also involved in clathrin-mediated endocytosis (By similarity).
!- PTM: Proteolytically processed under normal cellular conditions. Cleavage by alpha-secretase or alternatively by beta-secretase leads to generation and extracellular release of soluble APP peptides, S-APP-alpha and S-APP-beta, respectively, and the retention of corresponding membrane-anchored C-terminal fragments, C83 and C99. Subsequent processing of C83 by gamma-secretase yields P3 peptides. This is the major secretory pathway and is nonamyloidogenic. Alternatively, presenilin/nicastrin-mediated gamma-secretase processing of C99 releases the amyloid beta proteins, amyloid-beta 40 (Abeta40) and amyloid-beta 42 (Abeta42),

major components of amyloid plaques, and the cytotoxic C-terminal fragments, gamma-CTF(50), gamma-CTF(57) and gamma-CTF(59); (By similarity).

-!- PTM: Proteolytically cleaved by caspases during neuronal apoptosis (By similarity). Cleavage at Asp-739 by either caspase-3, 8 or -9 results in the production of the neurotoxic C31 peptide and the increased production of beta-amyloid peptides (By similarity).

-!- PTM: N- and O-glycosylated (By similarity).

-!- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and serine residues is neuron-specific. Phosphorylation can affect APP processing, neuronal differentiation and interaction with other proteins (By similarity).

-!- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and zinc, can induce histidine-bridging between beta-amyloid molecules resulting in beta-amyloid-metal aggregates (By similarity).

Extracellular zinc-binding increases binding of heparin to APP and inhibits collagen-binding (By similarity).

-!- SIMILARITY: Belongs to the APP family.

-!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.

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EMBL; M56727; AAA36829.1; -.
 EMBL; M56726; AAA36828.1; -.
 DR HSSP; P05067; 1AAP.
 DR InterPro; IPR008155; A4 APP.
 DR InterPro; IPR008154; A4 extra.
 DR InterPro; IPR001255; Beta-APP.
 DR InterPro; IPR002223; Kunitz_BPTI.
 DR Pfam; PF02177; A4_EXTRA; 1.
 DR Pfam; PF03494; Beta-APP; 1.
 DR Pfam; PF00014; Kunitz_BPTI; 1.
 DR PRINTS; PR00203; AMYLOIDA4.
 DR PRINTS; PR00759; BASICPTASE.
 DR ProDom; PD000222; Kunitz_BPTI; 1.
 DR SMART; SM00006; A4_EXTRA; 1.
 DR SMART; SM00131; K07; 1.
 DR PROSITE; PS00319; A4_EXTRA; 1.
 DR PROSITE; PS00320; A4_INTRA; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS00279; BPTI_KUNITZ_2; 1.
 KW Apoptosis; Endocytosis; Cell adhesion; Serine protease inhibitor;
 KW Coated pits; Neurone; Heparin-binding; Metal-binding; Copper; Iron;
 KW Zinc; Signal; Transmembrane; Glycoprotein; Phosphorylation;
 KW Proteoglycan; Alternative splicing; Amyloid.
 FT SIGNAL 1 17 BY SIMILARITY.
 FT CHAIN 18 770 AMYLOID BETA A4 PROTEIN.
 FT CHAIN 18 687 SOLUBLE APP-ALPHA (POTENTIAL).
 FT CHAIN 18 671 SOLUBLE APP-BETA (POTENTIAL).
 FT CHAIN 672 770 C99 (POTENTIAL).
 FT CHAIN 672 713 BETA-AMYLOID PROTEIN 42 (POTENTIAL).

672 711 CHAIN
 688 770 CHAIN
 688 713 CHAIN
 688 711 CHAIN
 712 770 CHAIN
 714 770 CHAIN
 721 770 CHAIN
 740 770 CHAIN
 18 699 FT DOMAIN
 700 723 FT TRANSMEM
 724 770 FT DOMAIN
 96 110 FT DOMAIN
 181 188 FT DOMAIN
 231 341 FT DOMAIN
 391 423 FT DOMAIN
 491 522 FT DOMAIN
 523 540 FT DOMAIN
 732 751 FT DOMAIN
 230 260 FT DOMAIN
 274 280 FT DOMAIN
 144 144 FT SITE
 301 302 FT ACT_SITE
 671 672 FT SITE
 672 673 FT SITE
 687 688 FT SITE
 704 704 FT SITE
 706 706 FT SITE
 711 712 FT SITE
 713 714 FT SITE
 720 721 FT SITE
 724 734 FT SITE
 739 740 FT SITE

BETA-AMYLOID PROTEIN 40 (POTENTIAL).
 C83 (POTENTIAL).
 P3(42) (POTENTIAL).
 P3(40) (POTENTIAL).
 GAMMA-CTF(59) (POTENTIAL).
 GAMMA-CTF(57) (POTENTIAL).
 GAMMA-CTF(50) (POTENTIAL).
 C31 (POTENTIAL).
 EXTRACELLULAR (POTENTIAL).
 POTENTIAL.
 CYTOPLASMIC (POTENTIAL).
 HEPARIN-BINDING (BY SIMILARITY).
 ZINC-BINDING (BY SIMILARITY).
 BPTI/KUNITZ INHIBITOR.
 HEPARIN-BINDING (BY SIMILARITY).
 HEPARIN-BINDING (BY SIMILARITY).
 COLLAGEN-BINDING (BY SIMILARITY).
 INTERACTION WITH G(I)-ALPHA
 (BY SIMILARITY).
 ASP/GLU-RICH (ACIDIC).
 POLY-THR.
 REQUIRED FOR COPPER(II) REDUCTION
 (BY SIMILARITY).
 REACTIVE BOND (BY SIMILARITY).
 CLEAVAGE (BY BETA-SECRETASE)
 (BY SIMILARITY).
 CLEAVAGE (BY CASPASE-6) (BY SIMILARITY).
 CLEAVAGE (BY ALPHA-SECRETASE)
 (BY SIMILARITY).
 IMPLICATED IN FREE RADICAL PROPAGATION
 (BY SIMILARITY).
 INVOLVED IN OXIDATIVE REACTIONS
 (BY SIMILARITY).
 CLEAVAGE (BY GAMMA-SECRETASE; SITE 1)
 (BY SIMILARITY).
 CLEAVAGE (BY GAMMA-SECRETASE; SITE 2)
 (BY SIMILARITY).
 CLEAVAGE (BY GAMMA-SECRETASE; SITE 3)
 (BY SIMILARITY).
 BASOLATERAL SORTING SIGNAL
 (BY SIMILARITY).
 CLEAVAGE (BY CASPASES-3,-6,-8 OR -9)

Query Match 100.0%; Score 52; DB 1; Length 770;
 Best Local Similarity 100.0%; Pred. No. 0.017;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KQYTSIHG 9
 |||||
 DB 726 KQYTSIHG 734

RESULT 6
 A4_MOUSE STANDARD; PRT; 770 AA.
 ID A4_MOUSE
 AC P12023; P57487; P97942; Q99K32;
 DT 01-OCT-1989 (Rel. 12, Created)

DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DE 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
 DE amyloid protein homology) (Amyloidogenic glycoprotein) (AG) (Contains:
 DE Soluble APP-alpha (S-APP-alpha); Soluble APP-beta (S-APP-beta); CS9
 DE (APP-C99); Beta-amyloid protein 42 (Beta-APP42); Beta-amyloid protein
 DE 40 (Beta-APP40); CS3; P3(42); P3(40); Gamma-CTF(59) (Gamma-secretase
 DE C-terminal fragment 59) (Amyloid intracellular domain 59) (AID(59))
 DE (APP-C59); Gamma-CTF(57) (Gamma-secretase C-terminal fragment 57)
 DE (Amyloid intracellular domain 57) (AID(57)); (APP-C57); Gamma-CTF(50)
 DE (Gamma-secretase C-terminal fragment 50) (Amyloid intracellular domain
 DE 50) (AID(50)); C311.
 GN APP.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CX NCBI_TaxID=10090;
 RN [1]
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM APP695).
 RC TISSUE=Brain;
 RX MEDLINE=88106489; PubMed=3322280;
 RA Yamada T., Sasaki H., Furuya H., Miyata T., Goto I., Sakaki Y.;
 RT "Complementary DNA for the mouse homolog of the human amyloid beta
 RT protein precursor.";
 RL Biochem. Biophys. Res. Commun. 149:665-671(1987).
 RN [2]
 RP REVISIONS.
 RA Yamada T.;
 RL Submitted (MAR-1988) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM APP695).
 RC STRAIN=BALE/c; TISSUE=Brain;
 RX MEDLINE=92096458; PubMed=1756177;
 RA de Strooper B., van Leeuwen F., van den Berghe H.;
 RT "The amyloid beta protein precursor or proteinase nexin II from mouse
 RT is closer related to its human homolog than previously reported.";
 RL Biochim. Biophys. Acta 1123:141-143(1991).
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM APP695).
 RC STRAIN=SAMP8; TISSUE=Hippocampus;
 RX MEDLINE=21130647; PubMed=11235921;
 RA Kumar V.B., Vyas K., Franko M., Choudhary V., Buddhiraju C.,
 RA Alvarez J., Morley J.E.;
 RT "Molecular cloning, expression, and regulation of hippocampal amyloid
 RT precursor protein of senescence accelerated mouse (SAMP8).";
 RL Biochem. Cell Biol. 79:57-67(2001).
 RN [5]
 RP SEQUENCE OF 1-19 FROM N.A.
 RX MEDLINE=92209998; PubMed=1555768;
 RA Izumi R., Yamada T., Yoshikai S.I., Sasaki H., Hattori M.,
 RA Sakai Y.;
 RT "Positive and negative regulatory elements for the expression of the
 RT Alzheimer's disease amyloid precursor-encoding gene in mouse.";
 RL Gene 112:189-195(1992).
 RN [6]
 RP PARTIAL SEQUENCE FROM N.A. (ISOFORM APP770).
 RC TISSUE=Breast tumor;
 RN [7]
 RP SEQUENCE OF 281-380 FROM N.A., AND ALTERNATIVE SPLICING.
 RC TISSUE=Brain, and Kidney;
 RX MEDLINE=89149813; PubMed=2493250;
 RA Yamada T., Sasaki H., Dohura K., Goto I., Sakaki Y.;
 RT "Structure and expression of the alternatively-spliced forms of mRNA
 RT for the mouse homolog of Alzheimer's disease amyloid beta protein
 RT precursor.";
 RL Biochem. Biophys. Res. Commun. 158:906-912(1989).
 RN [8]
 RP SEQUENCE OF 289-364 FROM N.A.
 RC STRAIN=CD-1; TISSUE=Placenta;
 RX MEDLINE=89345111; PubMed=2369710;
 RA Fukuchi K., Martin G.M., Deeb S.S.;
 RT "Sequence of the protease inhibitor domain of the A4 amyloid protein
 RT precursor of Mus domesticus.";
 RL Nucleic Acids Res. 17:5396-5396(1989).
 RN [9]
 RP SEQUENCE OF 656-737 FROM N.A.
 RC STRAIN=129/Sv;
 RA Wragg M.A., Busfield F., Duff K., Korenblatt K., Capocchi M.,
 RA Loring J.F., Goate A.M.;
 RT "Introduction of six mutations into the mouse genome using 'Hit and
 RT Run' gene-targeting: introduction of familial Alzheimer's disease
 RT mutations into the mouse amyloid precursor protein gene and
 RT humanization of the A-beta fragment.";
 RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
 RN [10]
 RP TISSUE SPECIFICITY OF ALTERNATIVE SPLICED FORMS.
 RX MEDLINE=93287808; PubMed=8105067;
 RA Sola C., Mengod G., Ghetti B., Palacios J.M., Triarhou L.C.;
 RT "Regional distribution of the alternatively spliced isoforms of beta
 RT APP RNA transcript in the brain of normal, heterozygous and
 RT homozygous weaver mutant mice as revealed by in situ hybridization
 RT histochemistry.";
 RL Brain Res. Mol. Brain Res. 17:340-346(1993).

RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.X.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Spapenon M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Frange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Rahy J., Helton E., Kettman M., Madañ A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Brakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [7]
 RP SEQUENCE OF 281-380 FROM N.A., AND ALTERNATIVE SPLICING.
 RC TISSUE=Brain, and Kidney;
 RX MEDLINE=89149813; PubMed=2493250;
 RA Yamada T., Sasaki H., Dohura K., Goto I., Sakaki Y.;
 RT "Structure and expression of the alternatively-spliced forms of mRNA
 RT for the mouse homolog of Alzheimer's disease amyloid beta protein
 RT precursor.";
 RL Biochem. Biophys. Res. Commun. 158:906-912(1989).
 RN [8]
 RP SEQUENCE OF 289-364 FROM N.A.
 RC STRAIN=CD-1; TISSUE=Placenta;
 RX MEDLINE=89345111; PubMed=2369710;
 RA Fukuchi K., Martin G.M., Deeb S.S.;
 RT "Sequence of the protease inhibitor domain of the A4 amyloid protein
 RT precursor of Mus domesticus.";
 RL Nucleic Acids Res. 17:5396-5396(1989).
 RN [9]
 RP SEQUENCE OF 656-737 FROM N.A.
 RC STRAIN=129/Sv;
 RA Wragg M.A., Busfield F., Duff K., Korenblatt K., Capocchi M.,
 RA Loring J.F., Goate A.M.;
 RT "Introduction of six mutations into the mouse genome using 'Hit and
 RT Run' gene-targeting: introduction of familial Alzheimer's disease
 RT mutations into the mouse amyloid precursor protein gene and
 RT humanization of the A-beta fragment.";
 RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
 RN [10]
 RP TISSUE SPECIFICITY OF ALTERNATIVE SPLICED FORMS.
 RX MEDLINE=93287808; PubMed=8105067;
 RA Sola C., Mengod G., Ghetti B., Palacios J.M., Triarhou L.C.;
 RT "Regional distribution of the alternatively spliced isoforms of beta
 RT APP RNA transcript in the brain of normal, heterozygous and
 RT homozygous weaver mutant mice as revealed by in situ hybridization
 RT histochemistry.";
 RL Brain Res. Mol. Brain Res. 17:340-346(1993).

RT "Amyloid precursor protein 770.";
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 1-136 FROM N.A.
 RC TISSUE=Small intestine;
 RA Winteroe A.K., Fredholm M.;
 RT "Evaluation and characterization of a porcine small intestine cDNA
 library.";
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE OF 667-723 FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=92017079; PubMed=1656157;
 RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
 RT "Conservation of the sequence of the Alzheimer's disease amyloid
 peptide in dog, polar bear and five other mammals by cross-species
 polymerase chain reaction analysis.";
 RL Brain Res. Mol. Brain Res. 10:299-303(1991).
 CC
 CC -!- FUNCTION: Functions as a cell surface receptor and performs
 CC physiological functions on the surface of neurons relevant to
 CC neurite growth, neuronal adhesion and axonogenesis. Involved in
 CC cell motility and transcription regulation through protein-protein
 CC interactions (By similarity). Can promote transcription activation
 CC through binding to APBB1/Tip60 and inhibit Notch signaling through
 CC interaction with Numb (By similarity). Couples to apoptosis-
 CC inducing pathways such as those mediated by G(O) and JIP (By
 CC similarity). Inhibits G(O) alpha ATPase activity (By similarity).
 CC Acts as a kinesin I membrane receptor, mediating the axonal
 CC transport of beta-secretase and presenilin 1 (By similarity). May
 CC be involved in copper homeostasis/oxidative stress through copper
 CC ion reduction (By similarity). In vitro, copper-metalated APP
 CC induces neuronal death directly or is potentiated through Cu(II)-
 CC mediated low-density lipoprotein oxidation (By similarity). Can
 CC regulate neurite outgrowth through binding to components of the
 CC extracellular matrix such as heparin and collagen I and IV (By
 CC similarity).
 CC -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
 CC with metal-reducing activity. Bind transient metals such as
 CC copper, zinc and iron (By similarity).
 CC -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
 CC peptides, including C31, are potent enhancers of neuronal
 CC apoptosis (By similarity).
 CC -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
 CC cytoplasmic proteins, including APBB family members, the APBA
 CC family, MAP6BP1, and SHC1, Numb and Dab1 (By similarity). Binding
 CC to Dab1 inhibits its serine phosphorylation (By similarity). Also
 CC interacts with GPCR-like protein BPP, FPRL1, APPBP1, IBI, KNS2
 CC (via its TPR domains) (By similarity), APPBP2 (via Bass) and DBP1.
 CC In vitro, it binds MAPT via the MT-binding domains (By
 CC similarity). Associates with microtubules in the presence of ATP
 CC and in a kinesin-dependent manner (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
 CC protein that rapidly becomes internalized via clathrin-coated
 CC pits. During maturation, the immature APP (N-glycosylated in the
 CC endoplasmic reticulum) moves to the Golgi complex where complete
 CC maturation occurs (O-glycosylated and sulfated). After alpha-
 CC secretase cleavage, soluble APP is released into the extracellular

space and the C-terminal is internalized to endosomes and
 lysosomes. Some APP accumulates in secretory transport vesicles
 leaving the late Golgi compartment and returns to the cell
 surface. Gamma-CTF(59) peptide is located to both the cytoplasm
 and nuclei of neurons (By similarity).
 -!- DOMAIN: The basolateral sorting signal (BASS) is required for
 sorting of membrane proteins to the basolateral surface of
 epithelial cells (By similarity).
 -!- DOMAIN: The NPXY sequence motif found in many tyrosine-
 phosphorylated proteins is required for the specific binding of
 the PID domain. However additional amino acids either N- or C-
 terminal to the NPXY motif are often required for complete
 interaction. The PID domain-containing proteins which bind APP
 require the YENPTY motif for full interaction. These interactions
 are independent of phosphorylation on the terminal tyrosine
 residue. The NPXY site is also involved in clathrin-mediated
 endocytosis (By similarity).
 -!- PTM: Proteolytically processed under normal cellular conditions.
 Cleavage by alpha-secretase or alternatively by beta-secretase
 leads to generation and extracellular release of soluble APP
 peptides, S-APP-alpha and S-APP-beta, respectively, and the
 retention of corresponding membrane-anchored C-terminal fragments,
 C83 and C99. Subsequent processing of C83 by gamma-secretase
 yields F3 peptides. This is the major secretory pathway and is
 nonamyloidogenic. Alternatively, presenilin/nicastrin-mediated
 gamma-secretase processing of C99 releases the amyloid beta
 proteins, amyloid-beta 40 (Abeta40) and amyloid-beta 42 (Abeta42),
 major components of amyloid plaques, and the cytotoxic C-terminal
 fragments, gamma-CTF(50), gamma-CTF(57) and gamma-CTF(59) (By
 similarity).
 -!- PTM: Proteolytically cleaved by caspases during neuronal apoptosis
 (By similarity). Cleavage at Asp-739 by either caspase-3, -8 or -9
 results in the production of the neurotoxic C31 peptide and the
 increased production of beta-amyloid peptides (By similarity).
 -!- PTM: N- and O-glycosylated (By similarity).
 -!- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and
 serine residues is neuron-specific. Phosphorylation can affect APP
 processing, neuronal differentiation and interaction with other
 proteins (By similarity).
 -!- PTM: Extracellular binding and reduction of copper, results in a
 corresponding oxidation of Cys-144 and Cys-158, and the formation
 of a disulfide bond (By similarity).
 -!- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and
 zinc, can induce histidine-bridging between beta-amyloid molecules
 resulting in beta-amyloid-metal aggregates (By similarity).
 Extracellular zinc-binding increases binding of heparin to APP and
 inhibits collagen-binding (By similarity).
 -!- SIMILARITY: Belongs to the APP family.
 -!- SIMILARITY: Contains 1 BPT1/Kunitz inhibitor domain.

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 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).

CC
 DR EMBL; AB032550; BA84580.1; --
 DR EMBL; Z84022; CA006313.1; --
 DR EMBL; X56127; CAA39592.1; --
 DR HSSP; P05067; IAAP.
 DR InterPro; IPR008153; A4_APP.
 DR InterPro; IPR008154; A4_extra.
 DR InterPro; IPR002223; Kunitz_BPTI.
 DR Pfam; PF02177; A4_EXTRA; 1.
 DR PRINTS; PR0203; AMYLOIDA4.
 DR PRINTS; PR0739; BASICPTASE.
 DR ProDom; PD000222; Kunitz_BPTI; 1.
 DR SMART; SM00006; A4_EXTRA; 1.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00319; A4_EXTRA; 1.
 DR PROSITE; PS00320; A4_INTRA; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS00279; BPTI_KUNITZ_2; 1.
 KW Apoptosis; Endocytosis; Cell adhesion; Serine protease inhibitor;
 KW Coated pits; Neurons; Heparin-binding; Metal-binding; Copper; Iron;
 KW Zinc; Signal; Transmembrane; Glycoprotein; Phosphorylation;
 KW Amyloid.
 FT SIGNAL 1 17 BY SIMILARITY.
 FT CHAIN 18 770 AMYLOID BETA A4 PROTEIN.
 FT CHAIN 18 687 SOLUBLE APP-ALPHA (POTENTIAL).
 FT CHAIN 18 671 SOLUBLE APP-BETA (POTENTIAL).
 FT CHAIN 672 770 C99 (BY SIMILARITY).
 FT CHAIN 672 713 BETA-AMYLOID PROTEIN 42 (BY SIMILARITY).
 FT CHAIN 672 711 BETA-AMYLOID PROTEIN 40 (BY SIMILARITY).
 FT CHAIN 688 770 C83 (BY SIMILARITY).
 FT CHAIN 688 713 P3(42) (BY SIMILARITY).
 FT CHAIN 688 711 P3(40) (BY SIMILARITY).
 FT CHAIN 712 770 GAMMA-CTF(59).
 FT CHAIN 714 770 GAMMA-CTF(57).
 FT CHAIN 721 770 GAMMA-CTF(50) (BY SIMILARITY).
 FT CHAIN 740 770 C31 (DURING APOPTOSIS) (BY SIMILARITY).
 FT CHAIN 18 699 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 700 723 POTENTIAL.
 FT CHAIN 724 770 CYTOPLASMIC (POTENTIAL).
 FT CHAIN 96 110 HEPARIN-BINDING (BY SIMILARITY).
 FT CHAIN 135 155 COPPER-BINDING (BY SIMILARITY).
 FT CHAIN 181 188 ZINC-BINDING (BY SIMILARITY).
 FT CHAIN 231 341 BPTI/KUNITZ INHIBITOR.
 FT CHAIN 391 423 HEPARIN-BINDING (BY SIMILARITY).
 FT CHAIN 491 522 HEPARIN-BINDING (BY SIMILARITY).
 FT CHAIN 523 540 COLLAGEN-BINDING (BY SIMILARITY).
 FT CHAIN 732 751 INTERACTION WITH G(O)-ALPHA (BY SIMILARITY).
 FT CHAIN 230 260 ASP/GLU-RICH (ACIDIC).
 FT CHAIN 274 280 POLY-THR.
 FT SITE 144 144 REQUIRED FOR COPPER(II) REDUCTION (BY SIMILARITY).
 FT ACT_SITE 301 302 REACTIVE BOND (BY SIMILARITY).
 FT SITE 671 672 CLEAVAGE (BY BETA-SECRETASE) (BY SIMILARITY).
 FT SITE 672 673 CLEAVAGE (BY CASPASE-6) (BY SIMILARITY).
 FT SITE 687 688 CLEAVAGE (BY ALPHA-SECRETASE)

FT SITE 704 704 (BY SIMILARITY).
 FT SITE 706 706 IMPLICATED IN FREE RADICAL PROPAGATION (BY SIMILARITY).
 FT SITE 711 712 INVOLVED IN OXIDATIVE REACTIONS (BY SIMILARITY).
 FT SITE 713 714 CLEAVAGE (BY GAMMA-SECRETASE; SITE 1) (BY SIMILARITY).
 FT SITE 720 721 CLEAVAGE (BY GAMMA-SECRETASE; SITE 2) (BY SIMILARITY).
 FT SITE 721 721 CLEAVAGE (BY GAMMA-SECRETASE; SITE 3) (BY SIMILARITY).
 Query Match 100.0%; Score 52; DB 1; Length 770;
 Best Local Similarity 100.0%; Pred. No. 0.017;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KQYTSIHG 9
 Db 726 KQYTSIHG 734
 RESULT 8
 A4_RAT ID A4_RAT STANDARD; PRT; 770 AA.
 AC P08592;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Amyloid beta A4 protein precursor (APP) (Alzheimer's disease amyloid protein homolog) (Amyloidogenic glycoprotein) (AG) (Contains: Soluble APP-alpha (S-APP-alpha); Soluble APP-beta (S-APP-beta); C99; Beta-amyloid protein 42 (Beta-APP42); Beta-amyloid protein 40 (Beta-APP40); C83; P3(42); P3(40); Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-CTF(57) (Gamma-secretase C-terminal fragment 57); Gamma-CTF(50) (Gamma-secretase C-terminal fragment 50); C31].
 GN APP.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM APP695).
 RC TISSUE=Brain;
 RX MEDLINE=88312583; PubMed=2900758;
 RA Shivers B.D., Hilbich C., Multhaup G., Salbaum J.M., Beyreuther K., Seeburg P.H.;
 RT "Alzheimer's disease amyloidogenic glycoprotein: expression pattern in rat brain suggests a role in cell contact."
 RL EMO J. 7:11365-1370(1988).
 RN [2]
 RP SEQUENCE OF 289-364 FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=89183625; PubMed=2648331;
 RA Kang J., Mueller-Hill B.;
 RT "The sequence of the two extra exons in rat preA4."
 RL Nucleic Acids Res. 17:2130-2130(1989).
 RN [3]
 RP SEQUENCE OF 720-730, AND MASS SPECTROMETRY.

RX MEDLINE=21443797; PubMed=11483588;
 RA Gu Y., Misonou H., Sato T., Dornae N., Takio K., Ihara Y.;
 RT "Distinct intramembrane cleavage of the beta-amyloid precursor protein
 family resembling gamma-secretase-like cleavage of Notch.";
 RL J. Biol. Chem. 276:35235-35238(2001).
 RN [4]
 RP ALTERNATIVE SPLICING.
 RX MEDLINE=96187032; PubMed=8624099;
 RA Sandbrink R., Masters C.L., Beyreuther K.;
 RT "APP gene family. Alternative splicing generates functionally related
 RT isoforms.";
 RL Ann. N.Y. Acad. Sci. 777:281-287(1996).
 RN [5]
 RP TISSUE SPECIFICITY OF APPICAN.
 RX MEDLINE=95263526; PubMed=7744833;
 RA Shioi J., Pangalos M.N., Ripellino J.A., Vassiliacopoulos D.,
 RA Mytilineou C., Margolis R.O., Robakis N.K.;
 RT "The Alzheimer amyloid precursor proteoglycan (appican) is present in
 RT brain and is produced by astrocytes but not by neurons in primary
 RT neural cultures.";
 RL J. Biol. Chem. 270:11839-11844(1995).
 RN [6]
 RP TISSUE SPECIFICITY OF ISOFORMS.
 RX MEDLINE=97150061; PubMed=8996834;
 RA Sandbrink R., Monning U., Masters C.L., Beyreuther K.;
 RT "Expression of the APP gene family in brain cells, brain development
 RT and aging.";
 RL Gerontology 43:119-131(1997).
 RN [7]
 RP INTERACTION WITH DBP1, AND MUTAGENESIS OF TYR-757; ASN-759 AND
 RP TYR-762.
 RX MEDLINE=99127916; PubMed=9307026;
 RA Watanabe T., Sukegawa J., Tomita S., Iijima K.-I., Oguchi S.,
 RA Suzuki T., Nairn A.C., Greengard P.;
 RT "A 127-kDa protein (UV-DBP) binds to the cytoplasmic domain of the
 RT Alzheimer's amyloid precursor protein.";
 RL J. Neurochem. 72:549-556(1999).
 RN [8]
 RP INTERACTION WITH GNAO1, AND MUTAGENESIS OF 732-HIS-HIS-733.
 RX MEDLINE=99162676; PubMed=10024356;
 RA Brouillet E., Tremblay A., Galanaud D., Volovitch M., Bouilliot C.,
 RA Valenza C., Prochiantz A., Allinquant B.;
 RT "The amyloid precursor protein interacts with Gq heterotrimeric
 RT protein within a cell compartment specialized in signal
 RT transduction.";
 RL J. Neurosci. 19:1717-1727(1999).
 RN [9]
 RP CHARACTERISTICS OF APPICAN, AND MUTAGENESIS OF SER-656.
 RX MEDLINE=95256193; PubMed=7737970;
 RA Pangalos M.N., Efthymiopoulos S., Shioi J., Robakis N.K.;
 RT "The chondroitin sulfate attachment site of appican is formed by
 RT splicing out exon 15 of the amyloid precursor gene.";
 RL J. Biol. Chem. 270:10388-10391(1995).
 RN [10]
 RP BETA-AMYLOID METAL-BINDING.
 RX MEDLINE=99316162; PubMed=10386999;
 RA Huang X., Atwood C.S., Hartshorn M.A., Multhaup G., Goldstein L.E.,
 RA Scarpa R.C., Quajjingo M.P., Gray D.N., Lim J., Moir R.D., Tanzi R.E.,
 RA Bush A.I.;
 RT "The A beta peptide of Alzheimer's disease directly produces hydrogen
 RT peroxide through metal ion reduction.";
 RL Biochemistry 38:7609-7616(1999).
 RN [11]
 RP BETA-AMYLOID ZINC BINDING.
 RX MEDLINE=99343552; PubMed=10413512;
 RA Liu S.-I., Howlett G., Barrow C.J.;
 RT "Histidine-13 is a crucial residue in the zinc ion-induced aggregation
 RT of the A beta peptide of Alzheimer's disease.";
 RL Biochemistry 38:9373-9378(1999).
 RN [12]
 RP IMPORTANCE OF GLY-704 IN FREE RADICAL PROPAGATION, AND MUTAGENESIS OF
 RP GLY-704.
 RX MEDLINE=21956095; PubMed=11959460;
 RA Kanski J., Vardarajan S., Aksanova M., Butterfield D.A.;
 RT "Role of glycine-33 and methionine-35 in Alzheimer's amyloid beta-
 RT peptide 1-42-associated oxidative stress and neurotoxicity.";
 RL Biochim. Biophys. Acta 1586:190-198(2001).
 RN [13]
 RP PHOSPHORYLATION.
 RX MEDLINE=97239592; PubMed=9085254;
 RA Oishi M., Nairn A.C., Czernik A.J., Lim G.S., Isohara T., Candy S.E.,
 RA Greengard P., Suzuki T.;
 RT "The cytoplasmic domain of Alzheimer's amyloid precursor protein is
 RT phosphorylated at Thr654, Ser655, and Thr668 in adult rat brain and
 RT cultured cells.";
 RL Mol. Med. 3:111-123(1997).
 RN [14]
 RP PHOSPHORYLATION ON SER-730.
 RX MEDLINE=99262094; PubMed=10293982;
 RA Isohara T., Horiuchi A., Watanabe T., Ando K., Czernik A.J., Uno I.,
 RA Greengard P., Nairn A.C., Suzuki T.;
 RT "Phosphorylation of the cytoplasmic domain of Alzheimer's beta-amyloid
 RT precursor protein at Ser655 by a novel protein kinase.";
 RL Biochem. Biophys. Res. Commun. 258:300-305(1999).
 RN [15]
 RP PHOSPHORYLATION, INDUCTION, SUBCELLULAR LOCATION, AND MUTAGENESIS OF
 RP THR-743.
 RX MEDLINE=99274744; PubMed=10341243;
 RA Ando K., Oishi M., Takeda S., Iijima K.-I., Isohara T., Nairn A.C.,
 RA Kirino Y., Greengard P., Suzuki T.;
 RT "Role of phosphorylation of Alzheimer's amyloid precursor protein
 RT during neuronal differentiation.";
 RL J. Neurosci. 19:4421-4427(1999).
 RN [16]
 RP PHOSPHORYLATION ON THR-743.
 RX MEDLINE=20396183; PubMed=10936190;
 RA Iijima K.-I., Ando K., Takeda S., Satoh Y., Seki T., Itohara S.,
 RA Greengard P., Kirino Y., Nairn A.C., Suzuki T.;
 RT "Neuron-specific phosphorylation of Alzheimer's beta-amyloid precursor
 RT protein by cyclin-dependent kinase 5.";
 RL J. Neurochem. 75:1085-1091(2000).
 RN [17]
 RP CARBOHYDRATE STRUCTURE OF APPICAN.
 RX MEDLINE=21463085; PubMed=11479316;

RA Tsuchida K., Shioi J., Yamada S., Boghosian G., Wu A., Cai H.,
 RA Sugahara K., Robakis N.K.;
 RT "Apocan, the proteoglycan form of the amyloid precursor protein,
 RT contains chondroitin sulfate E in the repeating disaccharide region";
 RL J. Biol. Chem. 276:37135-37160(2001).
 CC -!- FUNCTION: Functions as a cell surface receptor and performs
 CC physiological functions on the surface of neurons relevant to
 CC neurite growth, neuronal adhesion and axonogenesis. Involved in
 CC cell motility and transcription regulation through protein-protein
 CC interactions (By similarity). Can promote transcription activation
 CC through binding to APPS1/Tip60 and inhibit Notch signaling through
 CC interaction with Numb (By similarity). Couples to apoptosis-
 CC inducing pathways such as those mediated by G(O) and JIP. Inhibits
 CC G(O) alpha Affase activity. Acts as a kinesin I membrane receptor,
 CC mediating the axonal transport of beta-secretase and presenilin 1
 CC (By similarity). May be involved in copper homeostasis/oxidative
 CC stress through copper ion reduction. Can regulate neurite
 CC outgrowth through binding to components of the extracellular
 CC matrix such as heparin and collagen I and IV (By similarity). The
 CC splice isoforms that contain the BPTI domain possess protease
 CC inhibitor activity (By similarity).
 CC -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
 CC with metal-reducing activity. Bind transient metals such as
 CC copper, zinc and iron. Rat and mouse beta-amyloid peptides bind
 CC only weakly transient metals and have little reducing activity due
 CC to substitutions of transient metal chelating residues. Beta-APP42
 CC may activate mononuclear phagocytes in the brain and elicit
 CC inflammatory responses. Promotes both tau aggregation and TPX II-
 CC mediated phosphorylation (By similarity).
 CC -!- FUNCTION: Apicans elicit adhesion of neural cells to the
 CC extracellular matrix and may regulate neurite outgrowth in the
 CC brain.
 CC -!- FUNCTION: The gamma-CRF peptides as well as the caspase-cleaved
 CC peptides, including C31, are potent enhancers of neuronal
 CC apoptosis (By similarity).
 CC -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
 CC cytoplasmic proteins, including APBB family members, the APEA
 CC family, MAPK8IP1, SHC1 and Numb and Dab1 (By similarity). Binding
 CC to Dab1 inhibits its serine phosphorylation (By similarity). Also
 CC interacts with GPCR-like protein BPP, FPR1, APPBP1, IBI, KNS2
 CC (via its TPR domain), APPBP2 (via BASS) (By similarity) and DDB1.
 CC In vitro, it binds WAP1 via the MT-binding domains (By
 CC similarity). Associates with microtubules in the presence of ATP
 CC and in a kinesin-dependent manner (By similarity). Interacts,
 CC through a C-terminal domain, with GNAO1. Amyloid beta-42 binds
 CC CHRNA7 in hippocampal neurons (By similarity). Beta-amyloid
 CC associates with HADH2 (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
 CC protein that rapidly becomes internalized via clathrin-coated
 CC pits. During maturation, the immature APP (N-glycosylated in the
 CC pits. During maturation, the immature APP (N-glycosylated in the

Query Match 100.0% Score 52; DB 1; Length 770;
 Best Local Similarity 100.0%; Pred. No. 0.017;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KQYTSIRHG 9

Db 726 KQYTSIRHG 734
 |||||
 RESULT 9
 A4_TETFL
 ID A4_TETFL STANDARD; PRT; 780 AA.
 AC Q73683;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Alzheimer's disease amyloid A4 protein homolog precursor [Contains:
 DE Beta-amyloid protein (Beta-APP) (A-beta)].
 DE APP.
 GN APP.
 OS Tetraodon fluviatilis (Puffer fish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorphia; Tetraodontiformes;
 OC Tetraodontidae; Tetraodontidae; Tetraodon.
 OX NCBI_TaxID=47145;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=98252138; PubMed=9599080;
 RA Villard L., Tassone F., Crnogorac-Jurcovic T., Clancy K., Gardiner K.;
 RT "Analysis of pufferfish homologues of the A1-rich human APP gene.";
 RL Gene 210:17-24(1998).
 CC -!- FUNCTION: Functional neuronal receptor which couples to
 CC intracellular signaling pathway through the GTP-binding protein
 CC G(O) (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- SIMILARITY: Belongs to the APP family.
 CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL: AF018165; AAC41275.1; -.
 CC HSP: P03067; 1H23.
 CC InterPro: IPR008155; A4_APP.
 CC InterPro: IPR008154; A4_extra.
 CC InterPro: IPR001255; Beta-APP.
 CC InterPro: IPR002223; Kunitz_BPTI.
 CC Pfam: PF02177; A4_EXTRA; 1.
 CC Pfam: PF03494; Beta-APP; 1.
 CC Pfam: PF00014; Kunitz_BPTI; 1.
 CC PRINTS: PR00203; NWYLOIDM4.
 CC PRINTS: PR00739; BASICTPASE.
 CC ProDom: PD000222; Kunitz_BPTI; 1.
 CC SMART: SM00006; A4_EXTRA; 1.
 CC SMART: SM00131; KU; 1.
 CC PROSITE: PS00319; A4_EXTRA; 1.
 CC PROSITE: PS00320; A4_INTRA; 1.

DR PROSITE; PS00280; BPTI_KUNITZ_1; FALSE_NEG.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW Glycoprotein; Amyloid; Neurons; Transmembrane; Signal;
KW Serine protease inhibitor.

FT SIGNAL 1 18
FT CHAIN 19 780
FT CHAIN 682 724
FT DOMAIN 19 711
FT TRANSMEM 712 732
FT DOMAIN 733 780
FT DOMAIN 323 382
FT SITE 769 772
FT DISULFID 327 378
FT DISULFID 336 361
FT CARBOHYD 560 560
SQ SEQUENCE 780 AA; 38238 MW; 60071BE94520191D CRC64;

Query Match 100.0%; Score 52; DB 1; Length 780;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KQYTSIHGG 9
|||
Db 736 KQYTSIHGG 744

Search completed: October 4, 2004, 18:57:05
Job time : 10.4348 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model
Run on: October 4, 2004, 18:37:37 ; Search time 42.6522 Seconds
(without alignments)
66.577 Million cell updates/sec

Title: US-10-048-209-2
Perfect score: 52
Sequence: 1 KQYTSIHGG 9
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues
Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : SPTREMBL_25:*
- 1: sp_archaea:*
 - 2: sp_bacteria:*
 - 3: sp_fungi:*
 - 4: sp_human:*
 - 5: sp_invertebrate:*
 - 6: sp_mammal:*
 - 7: sp_mhc:*
 - 8: sp_organelle:*
 - 9: sp_phage:*
 - 10: sp_plant:*
 - 11: sp_rodent:*
 - 12: sp_virus:*
 - 13: sp_vertebrate:*
 - 14: sp_unclassified:*
 - 15: sp_virus:*
 - 16: sp_bacteriap:*
 - 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description

1 52 100.0 49 6 097917 Q8i58 chelydra se
2 52 100.0 113 13 Q8JH58 Q8bpv5 mus musculus
3 52 100.0 218 11 Q8BPV5 Q8ui7 brachydanio
4 52 100.0 237 13 Q8UI7 Q8ui8 brachydanio
5 52 100.0 357 13 Q8UI8 Q8bpc7 mus musculus
6 52 100.0 384 11 Q8BPC7 Q8uso0 brachydanio
7 52 100.0 472 13 Q8U50 Q83296 gallus gall
8 52 100.0 534 13 Q93296 Q8pvl1 gallus gall
9 52 100.0 569 13 Q9PVL1 Q919e7 brachydanio
10 52 100.0 612 13 Q919E7 Q7ztl brachydanio
11 52 100.0 578 13 Q7ZTL Q8urs brachydanio
12 52 100.0 594 13 Q8UR5 Q8jg8 gallus gall
13 52 100.0 695 13 Q9DGJ8 Q57394 narke japon
14 52 100.0 699 13 Q57394 Q8cw28 brachydanio
15 52 100.0 738 13 Q90W28 Q8cgj7 gallus gall
16 52 100.0 751 13 Q9DGJ7 Q8scq0 xenopus lae
17 49 94.2 693 13 Q9SG0 Q8sf9 xenopus lae
18 49 94.2 695 13 Q9SF9 Q7xq0 xenopus lae
19 49 94.2 695 13 Q7XQ0 Q1963 xenopus ap
20 49 94.2 747 13 Q91963 Q16020 homo sapien
21 45 86.5 82 4 Q16020 Q16014 homo sapien
22 45 86.5 82 4 Q16014 Q16019 homo sapien
23 45 86.5 82 4 Q16019 Q1743 brevicorone
24 37 71.2 133 5 Q1743 Q8ip90 bacillus an
25 37 71.2 164 16 Q8IP90 Q8ap0 bacteroides
26 37 71.2 228 16 Q8A0P0 Q92at6 listeria in
27 37 71.2 442 16 Q92AT6 Q9tw88 caenorhabdi
28 37 71.2 2584 5 Q9TW88 Q21920 caenorhabdi
29 37 71.2 2606 5 Q21920 Q83dx8 coxiella bu
30 36 69.2 71 16 Q83DX8 Q8cds5 mus musculus
31 36 69.2 116 11 Q8CDE5 Q8tr5 methanosarc
32 36 69.2 159 17 Q8TR5 Q8tr3 methanosarc
33 36 69.2 159 17 Q8TR3 Q8rx12 deinococcus
34 36 69.2 275 16 Q9RFX2 Q9cy29 spyrarena 1
35 36 69.2 333 13 Q90Y29 Q21806 caenorhabdi
36 36 69.2 412 5 Q21806 Q9za32 streptomyce
37 36 69.2 443 2 Q9ZA32 Q7vaj6 chara vulga
38 36 69.2 550 8 Q7YAJ6 Q8dkg0 synecococc
39 36 69.2 729 16 Q8DKG0 Q86uq4 homo sapien
40 36 69.2 5058 4 Q86UQ4 Q9xk5 bacillus ce
41 35 67.3 130 2 Q9XK5 Q9tmj3 clostridium
42 35 67.3 150 16 Q9TMJ3 Q7tpi2 peromyscus
43 35 67.3 210 11 Q7TPI2 Q8awr6 brachydanio
44 35 67.3 231 13 Q8AWR6 Q8lvkl bacillus an
45 35 67.3 277 16 Q8LVKL

ALIGNMENTS

RESULT 1
O97917 PRELIMINARY; PRT; 49 AA.
AC O97917;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE Amyloid protein (Fragment).
GN APP.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20063685; PubMed=10594237;
RA Konfortov B.A., Licence V.E., Miller J.R.;
RT "Resequencing of DNA from a diverse panel of cattle reveals a high
level of polymorphism in both intron and exon.";
RI Mamm. Genome 10:1142-1145(1999).
DR EMBL; AJ133033; CAB38017.1; -.
DR HSSP; P03067; 1BA4.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF03494; Beta-APP; 1.
FT NON_TER 1 49
FT NON_TER 49 49
SQ SEQUENCE 49 AA; 5183 MW; 6287463F0559BDED CRC64;

Query Match 100.0%; Score 52; DB 6; Length 49;
Best Local Similarity 100.0%; Pred. No. 0.0092;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KQYTSIHGG 9
DB 38 KQYTSIHGG 46

RESULT 2
Q8JH58 PRELIMINARY; PRT; 113 AA.
ID Q8JH58
AC Q8JH58;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Amyloid beta protein (Fragment).
OS Chelydra serpentina serpentina (common snapping turtle).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Testudines; Cryptodira; Testudinoidea; Chelydridae; Chelydra.
OX NCBI_TaxID=134619;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21876906; PubMed=11882478;
RA Trudeau V.L., Chiu S., Kennedy S.W., Brooks R.J.;
RT "Octylphenol (OP) alters the expression of members of the amyloid
protein family in the hypothalamus of the snapping turtle, Chelydra
serpentina serpentina.";
RI Environ. Health Perspect. 110:269-275(2002).
DR EMBL; AF541917; AAN04908.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR008155; A4 APP.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF03494; Beta-APP; 1.

DR PRINTS; PRO0203; AMYLOIDA4.
DR PROSITE; PS00320; A4_INTRA; 1.
FT NON_TER 1
SQ SEQUENCE 113 AA; 12750 MW; 72515C930496E053 CRC64;
Query Match 100.0%; Score 52; DB 13; Length 113;
Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KQYTSIHG 9
|||||
Db 69 KQYTSIHG 77
RESULT 3
QSBPV5 PRELIMINARY; PRT; 218 AA.
AC QSBPV5;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Amyloid beta (Fragment).
GN APP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK052448; BAC34997.1; -.
DR MGD; MGI:88659; App.
DR GO; GO:0005515; F:protein binding; IPI.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PRO0203; AMYLOIDA4.
DR PROSITE; PS00320; A4_INTRA; 1.
FT NON_TER 1
SQ SEQUENCE 218 AA; 24118 MW; 95B55AFDAE1D0BF5 CRC64;
Query Match 100.0%; Score 52; DB 11; Length 218;
Best Local Similarity 100.0%; Pred. No. 0.044;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KQYTSIHG 9
|||||
Db 174 KQYTSIHG 182
RESULT 4

QBUUI7 PRELIMINARY; PRT; 239 AA.
AC QBUUI7;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Putative membrane protein (fragment).
GN APPB.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX PubMed=11862463;
RA Musa A., Lehrach H., Russo V.E.A.;
RT "Distinct expression patterns of two zebrafish homologues of the human
RT App gene during embryonic development.";
RL Dev. Genes Evol. 211:563-567(2001).
DR EMBL; AJ315638; CAC85735.1; -.
DR ZFIN; ZDB-GENE-020220-1; appb.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PRO0203; AMYLOIDA4.
DR PROSITE; PS00320; A4_INTRA; 1.
FT NON_TER 1
SQ SEQUENCE 239 AA; 27048 MW; 8A69F746F821BAE2 CRC64;
Query Match 100.0%; Score 52; DB 13; Length 239;
Best Local Similarity 100.0%; Pred. No. 0.049;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KQYTSIHG 9
|||||
Db 195 KQYTSIHG 203
RESULT 5
QBUUI8 PRELIMINARY; PRT; 357 AA.
AC QBUUI8;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Putative membrane protein (fragment).
GN APPA.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.

RC TISSUE=Embryo;
RX PubMed=11862463;
RA Musa A., Lehrach H., Russo V.E.A.;
RT "Distinct expression patterns of two zebrafish homologues of the human
AP gene during embryonic development.";
RL Dev. Genes Evol. 211:563-567(2001).
DR EMBL; AJ315637; CAC85734.1; -.
DR ZFIN; ZDB-GENE-000616-13; appa.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR008155; A4_APP.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PROSITE; PS00320; A4_INTRA; 1.
FT NON_TER 1
SQ SEQUENCE 357 AA; 40962 MW; 07D99EEFC55B2D8 CRC64;
Query Match 100.0%; Score 52; DB 13; Length 357;
Best Local Similarity 100.0%; Pred.No. 0.075;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KQYTSIHGG 9
DB 313 KQYTSIHGG 321
|||||

RESULT 6
Q8BPC7 PRELIMINARY; PRT; 384 AA.
ID Q8BPC7
AC Q8BPC7;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Amyloid beta (Fragment).
GN APP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=22334663; PubMed=1466651;
RA The FANTOM Consortium,
RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs";
RL Nature 420:563-573(2002).
DR EMBL; AK076506; BAC36369.1; -.
DR MGD; MGI:98059; App.
DR GO; GO:0005515; F:protein binding; IPI.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PROSITE; PS00320; A4_INTRA; 1.
FT NON_TER 1

SQ SEQUENCE 384 AA; 43990 MW; A81B1AD8AE683173 CRC64;
Query Match 100.0%; Score 52; DB 11; Length 384;
Best Local Similarity 100.0%; Pred.No. 0.08;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KQYTSIHGG 9
DB 340 KQYTSIHGG 348
|||||

RESULT 7
Q8UUS0 PRELIMINARY; PRT; 472 AA.
ID Q8UUS0
AC Q8UUS0;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Putative membrane protein (Fragment).
GN APPA.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX PubMed=11862463;
RA Musa A., Lehrach H., Russo V.E.A.;
RT "Distinct expression patterns of two zebrafish homologues of the human
APP gene during embryonic development.";
RL Dev. Genes Evol. 211:563-567(2001).
DR EMBL; AJ315636; CAC85733.1; -.
DR ZFIN; ZDB-GENE-000616-13; appa.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PROSITE; PS00320; A4_INTRA; 1.
FT NON_TER 1
SQ SEQUENCE 472 AA; 53787 MW; 24F7128BE3356550 CRC64;
Query Match 100.0%; Score 52; DB 13; Length 472;
Best Local Similarity 100.0%; Pred.No. 0.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KQYTSIHGG 9
DB 428 KQYTSIHGG 436
|||||

RESULT 8
O93296 PRELIMINARY; PRT; 534 AA.
ID O93296
AC O93296;

DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Amyloid protein (Fragment).
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 CX NCBI_TaxID=9031;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98337885; PubMed=9671674;
 RA Barnes N.Y.; Li L.; Yoshikawa K.; Schwartz L.M.; Oppenheim R.W.;
 RA Milligan C.E.;
 RT "Increased production of amyloid precursor protein provides a
 RT substrate for caspase-3 in dying motoneurons."
 RL J. Neurosci. 18:5869-5880(1998).
 DR EMBL; AF042098; AAC25052.1; -.
 DR HSP; P05067; IBA4.
 DR GO; GO:0016020; C:membrane; IEA.
 DR InterPro; IPR008155; A4_APP.
 DR InterPro; IPR008154; A4_extra.
 DR InterPro; IPR001255; Beta-APP.
 DR Pfam; PF02177; A4_EXTRA; 1.
 DR Pfam; PF03494; Beta-APP; 1.
 DR PRINTS; PR0203; AMYLOIDA4.
 DR PROSITE; PS00319; A4_EXTRA; 1.
 DR PROSITE; PS00320; A4_INTRA; 1.
 DR NON_TER 1
 FT SEQUENCE 534 AA; 60597 MW; FB53EC2E6D4C92 CRC64;
 SQ SEQUENCE 534 AA; 60597 MW; FB53EC2E6D4C92 CRC64;

 Query Match 100.0%; Score 52; DB 13; Length 534;
 Best Local Similarity 100.0%; Pred. No. 0.11;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 1 KQYTSIHG 9
 Db 490 KQYTSIHG 498
 |||||

 RESULT 9
 Q9PVL1 PRELIMINARY; PRT; 569 AA.
 AC Q9PVL1
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Amyloid protein (Fragment).
 GN APP.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 CX NCBI_TaxID=9031;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;

RA Coulson E.J.; Paliga K.; Beyreuther K.; Masters C.L.;
 RT "What the evolution of the amyloid protein precursor supergene family
 RT tells us about its function."
 RL Neurochem. Int. 0:0-0(2000).
 DR EMBL; AF030341; AAF12698.1; -.
 DR HSP; P05067; IBA4.
 DR GO; GO:0016020; C:membrane; IEA.
 DR InterPro; IPR008155; A4_APP.
 DR InterPro; IPR008154; A4_extra.
 DR InterPro; IPR001255; Beta-APP.
 DR Pfam; PF02177; A4_EXTRA; 1.
 DR Pfam; PF03494; Beta-APP; 1.
 DR PRINTS; PR0203; AMYLOIDA4.
 DR PROSITE; PS00319; A4_EXTRA; 1.
 DR PROSITE; PS00320; A4_INTRA; 1.
 DR NON_TER 1
 FT SEQUENCE 569 AA; 64753 MW; 0AB8B851863A19D CRC64;
 SQ SEQUENCE 569 AA; 64753 MW; 0AB8B851863A19D CRC64;

 Query Match 100.0%; Score 52; DB 13; Length 569;
 Best Local Similarity 100.0%; Pred. No. 0.12;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 1 KQYTSIHG 9
 Db 526 KQYTSIHG 534
 |||||

 RESULT 10
 Q919E7 PRELIMINARY; PRT; 612 AA.
 AC Q919E7
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Amyloid protein (Fragment).
 GN APPA.
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 CX NCBI_TaxID=7955;
 RN (1)
 RP SEQUENCE FROM N.A.
 RA Slavov D.B.; Gardiner K.;
 RT "An App cDNA from Zebrafish (Danio rerio)."
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF257742; AAF1748.1; -.
 DR HSP; P05067; IHZ3.
 DR ZFIN; ZDB-GENE-000616-13; appa.
 DR GO; GO:0016020; C:membrane; IEA.
 DR InterPro; IPR008155; A4_APP.
 DR InterPro; IPR008154; A4_extra.
 DR InterPro; IPR001255; Beta-APP.
 DR Pfam; PF02177; A4_EXTRA; 1.
 DR Pfam; PF03494; Beta-APP; 1.
 DR PRINTS; PR0203; AMYLOIDA4.
 DR PROSITE; PS00319; A4_EXTRA; 1.

DR PROSITE; PS00320; A4_INTRA; 1.
 FT NON_TER 1
 SQ SEQUENCE 612 AA; 69710 MW; 59A9ACBDF9C59EFF CRC64;
 Query Match 100.0%; Score 52; DB 13; Length 612;
 Best Local Similarity 100.0%; Pred. No. 0.15;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KQYTSIHG 9
 |||||
 Db 568 KQYTSIHG 576
 RESULT 11
 Q7Z2T1 PRELIMINARY; PRT; 678 AA.
 ID Q7Z2T1
 AC Q7Z2T1
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Anyloid protein a variant 2.
 GN APPA.
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OC NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Groth C., Lardelli M.;
 RT "Investigation of zebrafish appa expression during embryogenesis.";
 RL Submitted (Apr-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY271746; AAP22958.1; -.
 DR GO; GO:0016020; C:membrane; IEA.
 DR InterPro; IPR008155; A4_APP.
 DR InterPro; IPR008154; A4_extra.
 DR InterPro; IPR001255; Beta-APP.
 DR Pfam; PF02177; A4_EXTRA; 1.
 DR Pfam; PF03494; Beta-APP; 1.
 DR PRINTS; PR00203; AMYLOIDA4.
 DR SMART; SM00006; A4_EXTRA; 1.
 DR PROSITE; PS00319; A4_EXTRA; 1.
 DR PROSITE; PS00320; A4_INTRA; 1.
 SQ SEQUENCE 678 AA; 76755 MW; 94163778444FD0BC CRC64;
 Query Match 100.0%; Score 52; DB 13; Length 678;
 Best Local Similarity 100.0%; Pred. No. 0.15;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KQYTSIHG 9
 |||||
 Db 634 KQYTSIHG 642
 RESULT 12
 Q8UUR9 PRELIMINARY; PRT; 694 AA.
 ID Q8UUR9

Q8UUR9;
 01-MAR-2002 (TrEMBLrel. 20, Created)
 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 Purative membrane protein.
 APPB.
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OC NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Musa A., Lehrach H., Russo V.E.A.;
 RT "Distinct expression patterns of two zebrafish homologues of the human
 Dev. Gene during embryonic development.";
 RL App. Genes Evol. 211:563-567(2001).
 DR EMBL; AJ315639; CAC85736.1; -.
 DR ZFIN; ZDB-GENE-020220-1; appb.
 DR GO; GO:0016020; C:membrane; IEA.
 DR InterPro; IPR008155; A4_APP.
 DR InterPro; IPR008154; A4_extra.
 DR InterPro; IPR001255; Beta-APP.
 DR Pfam; PF02177; A4_EXTRA; 1.
 DR Pfam; PF03494; Beta-APP; 1.
 DR PRINTS; PR00203; AMYLOIDA4.
 DR SMART; SM00006; A4_EXTRA; 1.
 DR PROSITE; PS00319; A4_EXTRA; 1.
 DR PROSITE; PS00320; A4_INTRA; 1.
 SQ SEQUENCE 694 AA; 79228 MW; 2B03382D41162DC CRC64;
 Query Match 100.0%; Score 52; DB 13; Length 694;
 Best Local Similarity 100.0%; Pred. No. 0.15;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KQYTSIHG 9
 |||||
 Db 650 KQYTSIHG 658
 RESULT 13
 Q9DGJ8 PRELIMINARY; PRT; 695 AA.
 ID Q9DGJ8
 AC Q9DGJ8;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Beta-amyloid precursor protein 695 isoform.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
 OC Gallus.
 OC NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.

SQ SEQUENCE 738 AA; 83577 MW; AF480F6D306FD298 CRC64;

Query Match 100.0%; Score 52; DB 13; Length 738;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KQYTSIHG 9

|||||||

Db 694 KQYTSIHG 702

Search completed: October 4, 2004, 18:56:21

Job time : 46.6522 secs

OM protein - protein search, using sw model
Run on: October 4, 2004, 18:37:13 ; Search time 58.0435 seconds
(without alignments)
48.679 Million cell updates/sec

Title: US-10-048-209-3
Perfect score: 57
Sequence: 1 KQYTSIHG 10
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 1586107 seqs, 282547505 residues
Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A.Geneseq.29Jan04:.*
1: geneseqp1980s:.*
2: geneseqp1990s:.*
3: geneseqp2000s:.*
4: geneseqp2001s:.*
5: geneseqp2002s:.*
6: geneseqp2003as:.*
7: geneseqp2003bs:.*
8: geneseqp2004s:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	57	100.0	12	AAB67793	Aab67793 Cytoplasm
2	57	100.0	13	AAB67794	Aab67794 Cytoplasm
3	57	100.0	15	AAB67798	Aab67798 Cytoplasm
4	57	100.0	19	ADC49255	Adc49255 Human inh
5	57	100.0	32	AA019883	Aaol9883 Human amy
6	57	100.0	33	ADC49254	Adc49254 Human inh
7	57	100.0	41	AAM16658	Aam16658 Peptide #
8	57	100.0	41	ABB35642	Abb35642 Peptide #
9	57	100.0	41	AAM29142	Aam29142 Peptide #

10	57	100.0	41	ABB30475	Abb30475 Peptide #
11	57	100.0	41	ABB21071	Abb21071 Protein #
12	57	100.0	41	AAM56458	Aam56458 Human bra
13	57	100.0	41	AAM04374	Aam04374 Peptide #
14	57	100.0	41	AEG38416	Aeg38416 Human pep
15	57	100.0	44	AAM53985	Aam53985 Human AL2
16	57	100.0	47	AAR58917	Aar58917 Cytoplasm
17	57	100.0	47	AAM26395	Aam26395 Amyloid p
18	57	100.0	47	AAM26402	Aam26402 Amyloid p
19	57	100.0	47	AAM26400	Aam26400 Amyloid p
20	57	100.0	47	AAM26403	Aam26403 Amyloid p
21	57	100.0	47	AAM26399	Aam26399 Amyloid p
22	57	100.0	47	AAM26401	Aam26401 Amyloid p
23	57	100.0	47	AAM26520	Aam26520 Amyloid p
24	57	100.0	47	AAM26518	Aam26518 Amyloid p
25	57	100.0	47	AAM26521	Aam26521 Amyloid p
26	57	100.0	47	AAM26519	Aam26519 Amyloid p
27	57	100.0	47	AAM26513	Aam26513 Amyloid p
28	57	100.0	47	AAM26517	Aam26517 Amyloid p
29	57	100.0	47	AAM42984	Aam42984 APP isofo
30	57	100.0	47	AAM42986	Aam42986 APP isofo
31	57	100.0	47	AAM42987	Aam42987 APP isofo
32	57	100.0	47	AAM42983	Aam42983 APP isofo
33	57	100.0	47	AAM42985	Aam42985 APP isofo
34	57	100.0	47	AAM44755	Aam44755 APP-REP 7
35	57	100.0	47	AAM44753	Aam44753 APP-REP 7
36	57	100.0	47	AAM44749	Aam44749 APP-REP 7
37	57	100.0	47	AAM44756	Aam44756 APP-REP 7
38	57	100.0	47	AAM44754	Aam44754 APP-REP 7
39	57	100.0	47	AAM44757	Aam44757 APP-REP 7
40	57	100.0	47	AAM44274	Aam44274 Amyloid p
41	57	100.0	47	AAB67791	Aab67791 Cytoplasm
42	57	100.0	47	ADC49250	Adc49250 Human inh
43	57	100.0	47	ADC49249	Adc49249 Inhibitor
44	57	100.0	47	ADC49251	Adc49251 Human inh
45	57	100.0	49	AAR35087	Aar35087 Human amy

ALIGNMENTS

RESULT 1
AAB67793
ID AAB67793 standard; peptide; 12 AA.
AC AAB67793;
XX
XX
DT 11-JUN-2001 (first entry)
XX
XX
Cytoplasmic domain of the amyloid protein precursor (APP).
XX
XX
Amyloid protein precursor; APP; apoptosis; cancer; Alzheimer's disease.
XX
XX
Homo sapiens.
XX
XX
Key Location/Qualifiers
FT Misc-difference 1

FT /note= "this residue represents an internalisation
 FT peptide such as the sequence given in AAB67795"
 FT Misc-difference 12
 FT /note= "this residue represents V, W, VVE, VVEV, VVEVD"
 FT
 XX
 PN WO200109170-A1.
 XX
 XX 08-FEB-2001.
 XX
 XX 28-JUL-2000; 2000WO-FR002174.
 XX
 XX 30-JUL-1999; 99FR-00009929.
 XX
 XX (CNRS) CNRS CENT NAT RECH SCI.
 XX
 XX Allinquant B, Prochiantz A;
 XX
 XX WPI; 2001-257398/26.
 XX
 XX Peptides derived from the cytoplasmic domain of the amyloid protein
 PT precursor, useful in the treatment of cancer and Alzheimer's disease.
 XX
 XX Claim 1; Page 13; 28pp; French.
 XX
 XX The present sequence represents a peptide derived from the cytoplasmic
 CC domain of the human amyloid protein precursor (APP). APP peptides derived
 CC from the cytoplasmic domain, and containing the membrane domain
 CC juxtaposed to the cytoplasmic domain of APP are useful for selecting and
 CC screening products capable of inhibiting apoptosis. The peptides are
 CC useful in the treatment of cancer and Alzheimer's disease
 XX
 SQ Sequence 12 AA;
 Query Match 100.0%; Score 57; DB 4; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.00082;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KKQYTSIHGG 10
 Db 2 KKQYTSIHGG 11
 RESULT 2
 AAB67794
 ID AAB67794 standard; peptide; 13 AA.
 XX
 AC AAB67794;
 XX
 XX 11-JUN-2001 (first entry)
 XX
 DE Cytoplasmic domain of the amyloid protein precursor (APP).
 XX
 XX Amyloid protein precursor; APP; apoptosis; cancer; Alzheimer's disease.
 XX
 OS Homo sapiens.
 XX
 PH Key Location/Qualifiers

FT Misc-difference 1
 FT /note= "this residue represents an internalisation
 FT peptide such as the sequence given in AAB67795"
 FT Misc-difference 13
 FT /note= "this residue represents V, W, VVE, VVEV, VVEVD"
 XX
 XX WO200109170-A1.
 XX
 XX 08-FEB-2001.
 XX
 XX 28-JUL-2000; 2000WO-FR002174.
 XX
 XX 30-JUL-1999; 99FR-00009929.
 XX
 XX (CNRS) CNRS CENT NAT RECH SCI.
 XX
 XX Allinquant B, Prochiantz A;
 XX
 XX WPI; 2001-257398/26.
 XX
 XX Peptides derived from the cytoplasmic domain of the amyloid protein
 PT precursor, useful in the treatment of cancer and Alzheimer's disease.
 XX
 XX Claim 1; Page 13; 28pp; French.
 XX
 XX The present sequence represents a peptide derived from the cytoplasmic
 CC domain of the human amyloid protein precursor (APP). APP peptides derived
 CC from the cytoplasmic domain, and containing the membrane domain
 CC juxtaposed to the cytoplasmic domain of APP are useful for selecting and
 CC screening products capable of inhibiting apoptosis. The peptides are
 CC useful in the treatment of cancer and Alzheimer's disease
 XX
 SQ Sequence 13 AA;
 Query Match 100.0%; Score 57; DB 4; Length 13;
 Best Local Similarity 100.0%; Pred. No. 0.00089;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KKQYTSIHGG 10
 Db 3 KKQYTSIHGG 12
 RESULT 3
 AAB67798
 ID AAB67798 standard; peptide; 15 AA.
 XX
 AC AAB67798;
 XX
 XX 11-JUN-2001 (first entry)
 XX
 DE Cytoplasmic domain of the amyloid protein precursor (APP).
 XX
 XX Amyloid protein precursor; APP; apoptosis; cancer; Alzheimer's disease.
 XX
 OS Homo sapiens.
 XX

PN WO200109170-A1.
 XX 09-FEB-2001.
 XX 28-JUL-2000; 2000WO-FR002174.
 PF 30-JUL-1999; 99FR-00009929.
 PR (CNRS) CNRS CENT NAT RECH SCI.
 XX Allinquant B, Prochiantz A;
 XX WPI; 2001-257398/26.
 XX Peptides derived from the cytoplasmic domain of the amyloid protein
 PT precursor, useful in the treatment of cancer and Alzheimer's disease.
 XX Disclosure; Page 2; 28pp; French.
 XX The present sequence represents a peptide derived from the cytoplasmic
 CC domain of the human amyloid protein precursor (APP). APP peptides derived
 CC from the cytoplasmic domain, and containing the membrane domain
 CC juxtaposed to the cytoplasmic domain of APP are useful for selecting and
 CC screening products capable of inhibiting apoptosis. The peptides are
 CC useful in the treatment of cancer and Alzheimer's disease
 XX
 SQ Sequence 15 AA;
 Query Match 100.0%; Score 57; DB 4; Length 15;
 Best Local Similarity 100.0%; Pred. No. 0.001;
 Matches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KKQYTSIHGG 10
 DB 2 KKQYTSIHGG 11
 RESULT 4
 ADC49255
 ID ADC49255 standard; protein; 19 AA.
 XX
 AC ADC49255;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Human inhibitor of metabolic degradation of APP variant #4.
 XX
 KW human; inhibitory factor; metabolic degradation of APP;
 KW amyloid precursor protein; Alzheimer's disease; mutant; mutein.
 XX
 OS Homo sapiens.
 XX
 PN JP2002360252-A.
 XX
 PD 17-DEC-2002.
 XX
 PF 27-APR-2001; 2001JP-00133178.

XX 27-APR-2001; 2001JP-00133178.
 PR (SUZU) SUZUKI T.
 PA (SUMU) SUMITOMO SEIYAKU KK.
 XX WPI; 2003-516151/49.
 DR An inhibitory factor of metabolic degradation of amyloid precursor
 PT protein (APP) which inhibits formation of beta-amyloid, useful in the
 PT treatment of Alzheimer's disease.
 XX Disclosure; SEQ ID NO 15; 33pp; Japanese.
 XX The invention relates to an inhibitory factor of metabolic degradation of
 CC APP. The factor is useful in the treatment of Alzheimer's disease. The
 CC present sequence is used in the exemplification of the invention.
 XX
 SQ Sequence 19 AA;
 Query Match 100.0%; Score 57; DB 7; Length 19;
 Best Local Similarity 100.0%; Pred. No. 0.0013;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KKQYTSIHGG 10
 DB 2 KKQYTSIHGG 11
 RESULT 5
 AAO19883
 ID AAO19883 standard; peptide; 32 AA.
 XX
 AC AAO19883;
 XX
 DT 11-AUG-2003 (first entry)
 XX
 DE Human amyloid precursor protein APP immunogenic peptide #3.
 XX
 KW Human; APP; amyloid precursor protein; immunogen; Alzheimer's disease;
 KW high-throughput screening; neuroprotective; nootropic; antiparkinsonian.
 XX
 OS Homo sapiens.
 XX
 PN WO2003001881-A2.
 XX
 PD 09-JAN-2003.
 XX
 PF 26-JUN-2002; 2002WO-US020267.
 XX
 PR 26-JUN-2001; 2001US-0300959p.
 XX
 PA (NYME-) NEW YORK STATE OFFICE MENTAL HEALTH.
 XX
 PI Mathews PM, Nixon RA, Schmidt SD, Jiang Y;
 XX WPI; 2003-210182/20.
 DR

XX Identifying compounds that modulates the generation of metabolites
PT associated with a disease or disorder, for treating e.g. Alzheimer's
PT disease by determining levels of a cellular component protein, or its
PT conformation state.
XX
PS Example 1; Page 29; 69pp; English.
XX
CC The present invention relates to a method of identifying compounds that
CC modulate the generation of one or more metabolites associated with a
CC disease or disorder comprising determining levels of a cellular component
CC protein or a conformation state of a cellular precursor protein. In
CC particular, the method can be used to determine levels of amyloid
CC precursor protein (APP), which is associated with Alzheimer's disease. It
CC is also useful for identifying compounds as drugs for treating diseases
CC or disorders associated with metabolic and/or proteolytic pathways, e.g.
CC Alzheimer's disease, Parkinson's disease, Huntington's disease, lysosomal
CC storage disorders, prion diseases, the tau-based neurodegenerative
CC disorders, and other non-AD amyloidoses. The present sequence is an
CC immunogenic portion of human APP
XX
SQ Sequence 32 AA;

Query Match 100.0%; Score 57; DB 6; Length 32;
Best Local Similarity 100.0%; Pred. No. 0.0024;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KQYTSIHGG 10
|||||
Db 6 KQYTSIHGG 15

RESULT 6
ADC49254
ID ADC49254 standard; protein; 33 AA.

XX ADC49254;
XX
XX DT 18-DEC-2003 (first entry)
XX DE Human inhibitor of metabolic degradation of APP variant #3.
XX KW human; inhibitor factor; metabolic degradation of APP;
XX KW amyloid precursor protein; Alzheimer's disease; mutant; mutein.

OS Homo sapiens.
XX JP2002360252-A.
XX PD 17-DEC-2002.
XX PF 27-APR-2001; 2001JP-00133178.
XX PR 27-APR-2001; 2001JP-00133178.
XX PA (SUZU/) SUZUKI T.
XX PA (SUMU) SUMITOMO SEIYAKU KK.

XX WPI; 2003-516151/49.
XX
XX PT An inhibitory factor of metabolic degradation of amyloid precursor
PT protein (APP) which inhibits formation of beta-amyloid, useful in the
PT treatment of Alzheimer's disease.
XX
XX PS Disclosure; SEQ ID NO 14; 33pp; Japanese.
XX
XX CC The invention relates to an inhibitory factor of metabolic degradation of
CC APP. The factor is useful in the treatment of Alzheimer's disease. The
CC present sequence is used in the exemplification of the invention.
XX
XX SQ Sequence 33 AA;

Query Match 100.0%; Score 57; DB 7; Length 33;
Best Local Similarity 100.0%; Pred. No. 0.0024;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KQYTSIHGG 10
|||||
Db 2 KQYTSIHGG 11

RESULT 7
AAMI6658
ID AAMI6658 standard; protein; 41 AA.

XX AAMI6658;
XX
XX DT 12-OCT-2001 (first entry)

XX DE Peptide #3092 encoded by probe for measuring cervical gene expression.
XX KW Probe; human; microarray; gene expression; cervical epithelial cell;
XX KW cervical cancer.

OS Homo sapiens.
XX WO200157278-A2.
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US000670.
XX PR 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 30-JUN-2000; 2000US-00608408.
XX PR 03-AUG-2000; 2000US-00632366.
XX PR 21-SEP-2000; 2000US-0234687P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX

DR WPI; 2001-489901/53.
XX Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human cervical epithelial cells.
XX
PS Claim 27; SEQ ID NO 21484; 487pp; English.
XX
CC The present invention relates to human single exon nucleic acid probes
CC (SENPs; see AA110068-AA128459). The present sequence is a peptide encoded
CC by one such probe. The SENPs are derived from human Hela cells. The SENPs
CC can be used to produce a single exon microarray, which can be used for
CC measuring human gene expression in a sample derived from human cervical
CC epithelial cells. By measuring gene expression, the probes are therefore
CC useful in grading and/or staging of diseases of the cervix, notably
CC cervical cancer. Note: The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 41 AA;
Query Match 100.0%; Score 57; DB 4; Length 41;
Best Local Similarity 100.0%; Pred. No. 0.0031;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KKQYTSIHGG 10
DB 29 KKQYTSIHGG 38
|||||
RESULT 8
ABB35642
ID ABB35642 standard; peptide; 41 AA.
XX
AC ABB35642;
XX
DT 04-FEB-2002 (first entry)
XX
DE Peptide #3148 encoded by human foetal liver single exon probe.
XX
KW Human; foetal liver; gene expression; single exon nucleic acid probe.
XX
OS Homo sapiens.
XX
PN WO200157277-A2.
XX
PD 09-AUG-2001.
XX
PE 30-JAN-2001; 2001WO-US000669.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX

PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-483447/52.
XX
XX Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human fetal liver.
XX
PS Claim 27; SEQ ID NO 28277; 639pp + Sequence Listing; English.
XX
CC The invention relates to a single exon nucleic acid probe for measuring
CC human gene expression in a sample derived from human foetal liver. The
CC single exon nucleic acid probes may be used for predicting, measuring and
CC displaying gene expression in samples derived from human fetal liver. The
CC present sequence is a peptide encoded by a single exon nucleic acid probe
CC of the invention. Note: The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 41 AA;
Query Match 100.0%; Score 57; DB 4; Length 41;
Best Local Similarity 100.0%; Pred. No. 0.0031;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KKQYTSIHGG 10
DB 29 KKQYTSIHGG 38
|||||
RESULT 9
AAM29142
ID AAM29142 standard; protein; 41 AA.
XX
AC AAM29142;
XX
DT 17-OCT-2001 (first entry)
XX
DE Peptide #3179 encoded by probe for measuring placental gene expression.
XX
KW Probe; microarray; human; placenta; antenatal diagnosis;
KW genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200157272-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000663.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX

PR 27-SEP-2000; 2000US-0236339P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 PA Penn SG, Hanzel DK, Chen W, Rank DR;
 XX WPI; 2001-488897/53.
 XX Human genome-derived single exon nucleic acid probes useful for analyzing
 PT gene expression in human placenta.
 PS Claim 27; SEQ ID NO 29411; 654pp; English.
 XX
 CC The present invention relates to single exon nucleic acid probes (SENPs;
 CC see AA131315-AA157546). The present sequence is a peptide encoded by one
 CC such probe. The probes are useful for producing a microarray for
 CC predicting, measuring and displaying gene expression in samples derived
 CC from human placenta. The probes are useful for antenatal diagnosis of
 CC human genetic disorders
 XX
 SQ Sequence 41 AA;
 Query Match 100.0%; Score 57; DB 4; Length 41;
 Best Local Similarity 100.0%; Pred. No. 0.0031;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KKQYTSIHG 10
 Db 29 KKQYTSIHG 38
 RESULT 10
 ABB30475
 ID ABB30475 standard; peptide; 41 AA.
 XX
 AC ABB30475;
 XX
 DT 01-FEB-2002 (first entry)
 XX
 DE Peptide #3126 encoded by breast cell single exon nucleic acid probe.
 XX
 KW Human; microarray; single exon probe; gene expression; breast; disease;
 KW cancer.
 XX
 OS Homo sapiens.
 XX
 PN W0200157271-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 30-JAN-2001; 2001WO-US000662.
 XX
 PR 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00606408.
 PR 03-AUG-2000; 2000US-00632366.

PR 21-SEP-2000; 2000US-02346897P.
 PR 27-SEP-2000; 2000US-0236339P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 PA Penn SG, Hanzel DK, Chen W, Rank DR;
 XX WPI; 2001-496933/54.
 XX New spatially-addressable set of single exon nucleic acid probes, useful
 PT for measuring gene expression in sample derived from human breast,
 PT comprises number of single exon nucleic acid probes.
 PS Claim 27; SEQ ID NO 13443; 327pp + Sequence Listing; English.
 XX
 CC The invention relates to a spatially-addressable set of single exon
 CC nucleic acid probes for measuring gene expression in a sample derived
 CC from human breast and BT 474 cells. The method involves contacting the
 CC probes with a collection of detectably labelled nucleic acids derived
 CC from mRNA of human breast, and then measuring the label bound to each
 CC probe of the microarray. The probes are useful for verifying the
 CC expression of regions of genomic DNA predicted to encode proteins. They
 CC are useful for gene discovery, and for determining predisposition and/or
 CC assessing the toxicity of chemical agents on cells. The microarray of
 CC this invention presents a far greater diversity of probes for measuring
 CC gene expression, with far less bias than expressed sequence tag
 CC microarrays. The method is suitable for rapid production of functional
 CC information from genomic sequence. The present sequence is a peptide
 CC encoded by a single exon nucleic acid probe of the invention. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 41 AA;
 Query Match 100.0%; Score 57; DB 4; Length 41;
 Best Local Similarity 100.0%; Pred. No. 0.0031;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KKQYTSIHG 10
 Db 29 KKQYTSIHG 38
 RESULT 11
 ABB21071
 ID ABB21071 standard; protein; 41 AA.
 XX
 AC ABB21071;
 XX
 DT 23-JAN-2002 (first entry)
 XX
 DE Protein #3070 encoded by probe for measuring heart cell gene expression.
 XX Human; gene expression; heart; microarray; vascular system;
 KW

KW cardiovascular disease; hypertension; cardiac arrhythmia;
KW congenital heart disease.

XX Homo sapiens.

XX W0200157274-A2.

XX 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US000666.

XX 04-FEB-2000; 2000US-0180312P.

XX 26-MAY-2000; 2000US-0207456P.

XX 30-JUN-2000; 2000US-00608408.

XX 03-AUG-2000; 2000US-00632366.

XX 21-SEP-2000; 2000US-0234687P.

XX 27-SEP-2000; 2000US-0236359P.

XX 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-488599/53.

XX Claim 15; SEQ ID NO 22841; 530pp; English.

XX The present invention relates to single exon nucleic acid probes for
XX measuring human gene expression in a sample derived from human heart (see
XX AB21335-ABA41305). The present sequence is a protein encoded by one such
XX probe. The probes may be used for predicting, measuring and displaying
XX gene expression in samples derived from the human heart via microarrays.
XX By measuring gene expression, the probes are useful for predicting,
XX diagnosing, grading, staging, monitoring and prognosing diseases of the
XX human heart and vascular system e.g. cardiovascular disease,
XX hypertension, cardiac arrhythmias and congenital heart disease. Note: The
XX sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pat_sequences

XX Sequence 41 AA;

SQ Sequence 41 AA;

Query Match 100.0%; Score 57; DB 4; Length 41;
Best Local Similarity 100.0%; Pred. No. 0.0031;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKQYTSIHGG 10

Db 29 KKQYTSIHGG 38

RESULT 12

AA56458

ID AA56458 standard; protein; 41 AA.

XX AA56458;

XX 05-NOV-2001 (First entry)

XX Human brain expressed single exon probe encoded protein SEQ ID NO: 28563.

XX Human; brain expressed exon; gene expression analysis; probe; microarray;

XX Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.

XX Homo sapiens.

XX W0200157275-A2.

XX 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US000667.

XX 04-FEB-2000; 2000US-0180312P.

XX 26-MAY-2000; 2000US-0207456P.

XX 30-JUN-2000; 2000US-00608408.

XX 03-AUG-2000; 2000US-00632366.

XX 21-SEP-2000; 2000US-0234687P.

XX 27-SEP-2000; 2000US-0236359P.

XX 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-483446/52.

XX Single exon nucleic acid probes for analyzing gene expression in human
XX brains.
XX Example 4; SEQ ID NO 28563; 650pp + Sequence Listing; English.
XX The present invention provides a number of single exon nucleic acid
XX probes which are derived from genomic sequences expressed in the human
XX brain. They can be used to measure gene expression in brain cell samples,
XX which may enable the diagnosis and improved treatment of nervous system
XX diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
XX epilepsy and cancers. The present sequence is a protein encoded by one of
XX the probes of the invention

SQ Sequence 41 AA;

Query Match 100.0%; Score 57; DB 4; Length 41;

Best Local Similarity 100.0%; Pred. No. 0.0031;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKQYTSIHGG 10

Db 29 KKQYTSIHGG 38

RESULT 13

AA04374
ID AA04374 standard; protein; 41 AA.
XX
AC AA04374;
XX
DT 09-OCT-2001 (first entry)
XX
DE Peptide #3056 encoded by probe for measuring breast gene expression.
XX
KW Probe; human; breast disease; breast cancer; development disorder;
XX inflammatory disease; proliferative breast disease; non-carcinoma tumour.
XX
OS Homo sapiens.
XX
PN W0200157270-A2.
XX
PD 09-AUG-2001.
XX
PF 29-JAN-2001; 2001WO-US0000661.
XX
PR 04-FEB-2000; 2000US-0180312P.
XX
PR 26-MAY-2000; 2000US-0207456P.
XX
PR 30-JUN-2000; 2000US-00608408.
XX
PR 03-AUG-2000; 2000US-00632366.
XX
PR 21-SEP-2000; 2000US-0234687P.
XX
PR 27-SEP-2000; 2000US-0236359P.
XX
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-476286/51.
XX
XX Novel single exon nucleic acid probe used to measuring gene expression in
PT a human breast.
XX
PS Claim 27; SEQ ID NO 13114; 322pp; English.
XX
CC The present invention relates to novel single exon nucleic acid probes
CC (see AA100010-AA110067). The present sequence is a peptide encoded by one
CC such probe. The probes are useful for measuring human gene expression in
CC a human breast sample, where the probe hybridises at high stringency to a
CC nucleic acid expressed in the human breast. The probes are useful for
CC predicting, diagnosing, grading, staging, monitoring and prognosing
CC diseases of the human breast, particularly those diseases with polygenic
CC aetiology. The diseases include: breast cancer, disorders of development,
CC inflammatory diseases of the breast, fibrocystic changes, proliferative
CC breast disease and non-carcinoma tumours. Note: The sequence data for
CC this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 41 AA;
XX
Query Match 100.0%; Score 57; DB 4; Length 41;
Best Local Similarity 100.0%; Pred. No. 0.0031;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KKQYTSIHG 10
|||||||
Db 29 KKQYTSIHG 38

RESULT 14
ABG38416
ID ABG38416 standard; peptide; 41 AA.
XX
AC ABG38416;
XX
DT 19-AUG-2002 (first entry)
XX
DE Human peptide encoded by genome-derived single exon probe SEQ ID 28081.
XX
KW Human; single exon probe; asthma; lung cancer; COPD; ILD;
KW chronic obstructive pulmonary disease; interstitial lung disease;
KW familial idiopathic pulmonary fibrosis; neurofibromatosis;
KW tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemorrhoidosis;
KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karagener syndrome;
KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
KW primary ciliary dyskinesia; pulmonary hypertension;
KW hyaline membrane disease.
XX
OS Homo sapiens.
XX
PN W0200186003-A2.
XX
PD 15-NOV-2001.
XX
PF 30-JAN-2001; 2001WO-US0000665.
XX
PR 04-FEB-2000; 2000US-0180312P.
XX
PR 26-MAY-2000; 2000US-0207456P.
XX
PR 30-JUN-2000; 2000US-00608408.
XX
PR 03-AUG-2000; 2000US-00632366.
XX
PR 21-SEP-2000; 2000US-0234687P.
XX
PR 27-SEP-2000; 2000US-0236359P.
XX
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2002-114183/15.
XX
XX Spatially-addressable set of single exon nucleic acid probes, used to
PT measure gene expression in human lung samples.
XX
PS Claim 27; SEQ ID NO 28081; 634pp; English.
XX
CC The invention relates to a spatially-addressable set of single exon
CC nucleic acid probes for measuring gene expression in a sample derived
CC from human lung comprising single exon nucleic acid probes having one of

CC 12614 nucleic acid sequences mentioned in the specification, or their
 CC complements or the 12387 open reading frames derived from the 12614
 CC probes. Also included are a microarray comprising the novel set of probes
 CC ; the novel set of probes which hybridise at high stringency to a nucleic
 CC acid expressed in the human lung; measuring gene expression in a sample
 CC derived from human lung, comprising (a) contacting the array with a
 CC collection of detectably labeled nucleic acids derived from human lung
 CC mRNA, and (b) measuring the label detectably bound to each probe of the
 CC array; identifying exons in a eukaryotic genome, comprising (a)
 CC algorithmically predicting at least one exon from genomic sequences of
 CC the eukaryote; and (b) detecting specific hybridisation of detectably
 CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,
 CC having a fragment identical to the predicted exon, the probe is included
 CC in the above mentioned microarray; assigning exons to a single gene,
 CC comprising (a) identifying exons from genomic sequence by the method
 CC above and (b) measuring the expression of each of the exons in several
 CC tissues and/or cell types using hybridisation to a single exon
 CC microarrays having a probe with the exon, where a common pattern of
 CC expression of the exons in the tissues and/or cell types indicates that
 CC the exons should be assigned to a single gene; a peptide comprising one
 CC of 12011 sequences, mentioned in the specification, or encoded by the
 CC probes/open reading frames (ORF). The probes are used for gene expression
 CC analysis, and for identifying exons in a gene, particularly using human
 CC lung derived mRNA and for the study of lung diseases such as asthma, lung
 CC cancer, chronic obstructive pulmonary disease (COPD), interstitial lung
 CC disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,
 CC tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-
 CC Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary
 CC histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis,
 CC Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary
 CC dyskinesia, pulmonary hypertension and hyaline membrane disease. The
 CC present sequence is a peptide/protein encoded by a single exon probe of
 CC the invention. Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 XX

SQ Sequence 41 AA;

Query Match 100.0%; Score 57; DB 5; Length 41;
 Best Local Similarity 100.0%; Pred. No. 0.0031;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KQYTSIHG 10
 |||||
 Db 29 KQYTSIHG 38

RESULT 15
 AAW53985
 ID AAW53985 standard; protein; 44 AA.
 XX
 XX AAW53985;
 AC

DT 18-AUG-1998 (first entry)
 XX
 DE Human ALZASp2.
 XX

KW Dsas; DSASP; alzaz; Down's syndrome; diagnosis; therapy; human;
 KW Alzheimer's disease.
 XX
 OS Homo sapiens.
 XX
 PN WO9807850-A2.
 XX
 PD 26-FEB-1998.
 XX
 XX 22-AUG-1997; 97WO-EP004599.
 PF
 XX 22-AUG-1996; 96CA-02183901.
 PR
 XX (BERG/) BERGMANN J E.
 PA (PRED/) FREDDIE E R.
 XX
 PI Bergmann JE, Freddie ER;
 XX
 XX WPI; 1998-169155/15.
 DR
 XX N-PSDB; AAV23755.
 DR
 XX Nucleic acid molecules dsas, and alzaz - used for detecting and treating
 PT Down's syndrome and Alzheimer's disease.
 PT
 XX Claim 13; Fig 1M; 96pp; English.
 XX
 PS This sequence is the ALZASp2 encoded by the nucleic acid alzaz. The dsas
 CC and alzaz DNA sequences are the nucleic acids of the invention. Reagents
 CC specifically for DSASP can be used for the diagnosis of Down's syndrome
 CC in humans and especially in pregnant women. Molecules that inhibit the
 CC activity of the promoters (PDS1, PDS2, and PDS4) for dsas can be
 CC used for treating Down's syndrome. The reagent capable of detecting alzaz
 CC can be used for detecting Alzheimer's disease, especially in the pre-
 CC symptomatic stage. Substances that inhibit the promoters for alzaz can be
 CC used in treating Alzheimer's disease
 CC
 XX Sequence 44 AA;

Query Match 100.0%; Score 57; DB 2; Length 44;
 Best Local Similarity 100.0%; Pred. No. 0.0033;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KQYTSIHG 10
 |||||
 Db 20 KQYTSIHG 29

Search completed: October 4, 2004, 18:52:36
 Job time : 58.0435 secs

OM protein - protein search, using sw model

Run on: October 4, 2004, 18:45:55 ; Search time 14.7826 seconds
(without alignments)
65.071 Million cell updates/sec

Title: US-10-048-209-3
Perfect score: 57
Sequence: 1 KQVTSIHG 10

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:
1: pir1:
2: pir2:
3: pir3:
4: pir4:

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	57	100.0	82	2 PQ0438	Alzheimer's disease
2	57	100.0	695	1 A49795	Alzheimer's disease
3	57	100.0	695	2 A27485	Alzheimer's disease
4	57	100.0	695	2 S00550	Alzheimer's disease
5	57	100.0	770	1 QRHUA4	Alzheimer's disease
6	54	94.7	747	2 JH0773	Alzheimer's disease
7	39	68.4	452	2 S58994	NADH2 dehydrogenas
8	38	66.7	406	2 S76307	hypothetical prote
9	38	66.7	488	2 S64140	hypothetical prote
10	37	64.9	142	2 T10871	y4kQ protein - Rhi
11	37	64.9	442	2 AH1661	ATP-dependent RNA
12	37	64.9	2584	2 T24158	hypothetical prote
13	37	64.9	2606	2 T24157	hypothetical prote

14	36	63.2	275	2 C75529	competence protein
15	36	63.2	412	2 T24023	hypothetical prote
16	36	63.2	443	2 T46532	probable cAMP-4-ke
17	36	63.2	1268	2 B86209	protein K0Z42.6 [i
18	36	63.2	1313	2 T29193	hypothetical prote
19	35	61.4	150	2 F96924	flavodoxin (import
20	35	61.4	191	2 A35981	sperm membrane pro
21	35	61.4	239	2 T01463	hypothetical prote
22	35	61.4	264	2 T15289	hypothetical prote
23	35	61.4	410	2 A11660	aminopeptidases ho
24	35	61.4	410	2 AG1258	aminopeptidases ho
25	35	61.4	443	2 B39794	transcription fact
26	35	61.4	444	1 A39794	transcription fact
27	35	61.4	452	2 T04781	hypothetical prote
28	35	61.4	511	2 JC1404	CDEI-bbox DNA-bindi
29	35	61.4	522	2 A83804	involved in spore
30	35	61.4	739	2 AG1667	phosphoribosylform
31	35	61.4	739	2 A11295	phosphoribosylform
32	35	61.4	751	2 A49974	beta-amyloid precu
33	35	61.4	763	2 A49321	amyloid beta (A4)
34	35	61.4	765	2 S42880	amyloid precursor-
35	35	61.4	848	2 E85087	hypothetical prote
36	34	59.6	99	2 B82524	hypothetical prote
37	34	59.6	100	2 T41338	very hypothetical
38	34	59.6	119	2 AG3136	hypothetical prote
39	34	59.6	254	2 T28556	hypothetical prote
40	34	59.6	332	2 T23779	transcription fact
41	34	59.6	344	1 TWXL3	nitrogen regulatio
42	34	59.6	348	2 S23900	hypothetical prote
43	34	59.6	393	2 C96592	permease (imported
44	34	59.6	409	2 C96956	hypothetical prote
45	34	59.6	637	2 H70535	hypothetical prote

ALIGNMENTS

RESULT 1

PQ0438
Alzheimer's disease amyloid A4 protein precursor - rabbit (fragment)
C/Species: Oryctolagus cuniculus (domestic rabbit)
C/Date: 30-Sep-1993 #sequence_revision 19-Oct-1995 #text_change 19-Oct-1995
C/Accession: PQ0438; C60045
R/Davidson, J.S.; West, R.L.; Kotikalapudi, P.; Maroun, L.E.
Biochem. Biophys. Res. Commun. 188, 905-911, 1992
A/Title: Sequence and methylation in the beta/A4 region of the rabbit amyloid
precursor protein gene.
A/Reference number: PQ0438; MUID:93075180; PMID:1445331
A/Accession: PQ0438
A/Molecule type: DNA
A/Residues: 1-82 <DAV>
A/Cross-references: GB:MB3558; GB:MB3657
R/Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A/Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide
in dog, polar bear and five other mammals by cross-species polymerase chain
reaction analysis.

A/Reference number: A60045; MUID:92017079; PMID:1656157
A/Accession: C60045
A/Molecule type: mRNA
A/Residues: 12-68 <UOH>
A/Cross-references: EMBL:X56129
C/Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type
C/Keywords: alternative splicing; Alzheimer's disease; amyloid; Down's syndrome

Query Match 100.0%; Score 57; DB 2; Length 82;
Best Local Similarity 100.0%; Pred. No. 0.0089;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KQYTSIHG 10
|||||
Db 70 KQYTSIHG 79

RESULT 2
A49795
Alzheimer's disease amyloid beta protein precursor - crab-eating macaque
C/Species: Macaca fascicularis (crab-eating macaque)
C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C/Accession: A49795
R/Polidary, M.B.; Tolan, D.R.; Selkoe, D.J.
Am. J. Pathol. 138, 1423-1435, 1991
A/Title: Homology of the amyloid beta protein precursor in monkey and human supports a primate model for beta amyloidosis in Alzheimer's disease.
A/Reference number: A49795; MUID:91273117; PMID:1905108
A/Accession: A49795
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-695 <POD>
C/Cross-references: GB:M58727; NID:g342062; PIDN:AAA36829.1; PID:g342063
C/Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type
C/Keywords: alternative splicing

Query Match 100.0%; Score 57; DB 1; Length 695;
Best Local Similarity 100.0%; Pred. No. 0.0089;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KQYTSIHG 10
|||||
Db 650 KQYTSIHG 659

RESULT 3
A27485
Alzheimer's disease amyloid beta/A4 protein homolog precursor - mouse
N/Alternate names: proteinase nexin II
C/Species: Mus musculus (house mouse)
C/Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 13-Aug-1999
C/Accession: A27485; S19727; I49485
R/Yamada, T.; Sasaki, H.; Furuya, H.; Miyata, T.; Goto, I.; Sasaki, Y.
Biochem. Biophys. Res. Commun. 149, 668-671, 1987

A/Title: Complementary DNA for the mouse homolog of the human amyloid beta protein precursor.
A/Reference number: A27485; MUID:88106489; PMID:3322280
A/Accession: A27485
A/Molecule type: mRNA
A/Residues: 1-695 <FAH>
A/Cross-references: GB:M18373; NID:g191568; PIDN:AAA37139.1; PID:g309085
A/Experimental source: brain
R/de Strooper, B.; van Leeuwen, F.; van den Berghe, H.
Biochim. Biophys. Acta 1129, 141-143, 1991
A/Title: The amyloid beta protein precursor or proteinase nexin II from mouse is closer related to its human homolog than previously reported.
A/Reference number: S19727; MUID:92096436; PMID:1756177
A/Accession: S19727
A/Molecule type: mRNA
A/Residues: 1-210, 'G', 212-220, 'S', 222-396, 'A', 398-402, 'T', 404-448, 'A', 450-695 <STR>
A/Cross-references: EMBL:X59379
R/Izumi, R.; Yamada, T.; Yoshikai, S.; Sasaki, H.; Hattori, M.; Sasaki, Y.
Gene 112, 189-195, 1992
A/Title: Positive and negative regulatory elements for the expression of the Alzheimer's disease amyloid precursor-encoding gene in mouse.
A/Reference number: I49485; MUID:92209998; PMID:1555768
A/Accession: I49485
A/Status: translated from GB/ENBL/DBJ
A/Molecule type: DNA
A/Residues: 1-19 <RES>
A/Cross-references: GB:DI0603; NID:g220328; PIDN:BAA01456.1; PID:g220329
C/Genetics:
A/Map position: 16C3
C/Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type
C/Keywords: alternative splicing; amyloid; transmembrane protein

Query Match 100.0%; Score 57; DB 2; Length 695;
Best Local Similarity 100.0%; Pred. No. 0.0089;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KQYTSIHG 10
|||||
Db 650 KQYTSIHG 659

RESULT 4
S00550
Alzheimer's disease amyloid beta protein precursor - rat
N/Alternate names: beta-A4 amyloid protein
C/Species: Rattus norvegicus (Norway rat)
C/Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 13-Aug-1999
C/Accession: S00550; A41245; A39820; S46251
R/Shivers, B.D.; Hilbich, C.; Multhaup, G.; Salbaum, M.; Beyreuther, K.; Seeburg, P.H.
EMBO J. 7, 1365-1370, 1988
A/Title: Alzheimer's disease amyloidogenic glycoprotein: expression pattern in rat brain suggests a role in cell contact.
A/Reference number: S00550; MUID:88312583; PMID:2900758
A/Accession: S00550

S06121; A60355; A59011; A39384; S29076; S38252; S32539; S48148; S48592; S51186; S51185; S51184; S51183; A54238; I58075; I52250; S09010; S10737; S24127; S43644
 R.Lemaire, H.G.; Salbaum, J.M.; Multhaup, G.; Kang, J.; Bayney, R.M.; Unterbeck, A.; Beyreuther, K.; Mueller-Hill, B.
 Nucleic Acids Res. 17, 517-522, 1989
 A>Title: The PreA4(695) precursor protein of Alzheimer's disease A4 amyloid is encoded by 16 exons.
 A/Reference number: S02260; MUID:89128427; PMID:2783775
 A/Accession: S02260
 A/Molecule type: DNA
 A/Residues: 1-288, IV', 365-770 <LEM1>
 A/Cross-references: EMBL:X13466
 A/Note: alternative splice form APP(695)
 R.Lemaire, H.G.
 submitted to the EMBL Data Library, November 1988
 A/Reference number: S05194
 A/Accession: S05194
 A/Molecule type: DNA
 A/Residues: 1-14, 'VM', 17-288, IV', 365-770 <LEM2>
 A/Cross-references: EMBL:X13466; NID:g35598; PIDN:CAA31830.1; PID:g871360
 A/Note: alternative splice form APP(695)
 R.La Fauci, G.; Lahiri, D.K.; Salton, S.R.J.; Robakis, N.K.
 Biochem. Biophys. Res. Commun. 159, 297-304, 1989
 A>Title: Characterization of the 5'-end region and the first two exons of the beta-protein precursor gene.
 A/Reference number: A32277; MUID:89165870; PMID:2538123
 A/Accession: A32277
 A/Molecule type: DNA
 A/Residues: 1-75 <LAF>
 A/Cross-references: GB:M24547; NID:g341202; PIDN:AA013654.1; PID:g516074
 R.Johnstone, E.M.; Chaney, M.O.; Moore, R.E.; Ward, K.E.; Norris, F.H.; Little, S.P.
 Biochem. Biophys. Res. Commun. 163, 1248-1255, 1989
 A>Title: Alzheimer's disease amyloid peptide is encoded by two exons and shows similarity to soybean trypsin inhibitor.
 A/Reference number: A33260; MUID:89392030; PMID:2675837
 A/Accession: A33260
 A/Molecule type: DNA
 A/Residues: 656-737 <JOH>
 A/Cross-references: GB:M29270; NID:g178863; PIDN:AAA31768.1; PID:g178865
 R.Prelli, F.; Levy, E.; van Duinen, S.G.; Bots, G.T.A.M.; Luyendijk, W.; Frangione, B.
 Biochem. Biophys. Res. Commun. 170, 301-307, 1990
 A>Title: Expression of a normal and variant Alzheimer's beta-protein gene in amyloid of hereditary cerebral hemorrhage, Dutch type: DNA and protein diagnostic assays.
 A/Reference number: A35486; MUID:90321244; PMID:2196878
 A/Accession: A35486
 A/Molecule type: DNA
 A/Residues: 672-710 <PREL>
 A/Note: 693-Gln was found in DNA isolated from HCMA-D patients
 R.Yoshikai, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sakaki, Y.
 Gene 87, 257-263, 1990
 A>Title: Genomic organization of the human amyloid beta-protein precursor gene.
 A/Reference number: I39451; MUID:90236318; PMID:2110105
 A/Accession: I39452

A/Molecule type: mRNA
 A/Residues: 1-655 <SH>
 A/Cross-references: EMBL:X07648; NID:g55616; PIDN:CAA30488.1; PID:g55617
 R.Schubert, D.; Schroeder, R.; LaCorbiere, M.; Saitoh, T.; Cole, G.
 Science 241, 223-226, 1988
 A>Title: Amyloid beta protein precursor is possibly a heparan sulfate proteoglycan core protein.
 A/Reference number: A41245; MUID:88264430; PMID:2568652
 A/Accession: A41245
 A/Molecule type: protein
 A/Residues: 18-37, 'X', 39-40, 'X', 42-44 <SCH>
 A/Note: evidence for heparan sulfate attachment
 R.Hesse, L.; Behr, D.; Masters, C.L.; Multhaup, G.
 FEBS Lett. 349, 109-116, 1994
 A>Title: The beta-A4 amyloid precursor protein binding to copper.
 A/Reference number: A46251; MUID:94320627; PMID:7913895
 A/Contents: annotation; copper binding sites
 A/Note: rat peptides were isolated but not sequenced
 R.Petemeska, A.; Styles, J.; Menta, P.; Kim, K.S.; Miller, D.L.
 J. Biol. Chem. 266, 8464-8469, 1991
 A>Title: Purification and tissue level of the beta-amyloid peptide precursor of rat brain.
 A/Reference number: A39820; MUID:91217087; PMID:1673681
 A/Accession: A39820
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 18-32 <POT>
 A/Experimental source: brain
 C/Comment: Deposition of amyloid protein as neurofibrillary tangles and/or plaques is characteristic of both Alzheimer's disease and Down's syndrome.
 C/Suprafamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase inhibitor homology
 C/Keywords: alternative splicing; amyloid; glycoprotein; transmembrane protein
 F:625-648/Domain: transmembrane #status predicted <TM>
 Query Match 100.0%; Score 57; DB 2; Length 695;
 Best Local Similarity 100.0%; Pred. No. 0.0089;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KQYTSIHG 10
 |||||
 Db 650 KQYTSIHG 659
 RESULT 5
 QRU04
 Alzheimer's disease amyloid beta protein precursor [validated] - human
 N/Alternate names: Alzheimer's disease amyloid A4 protein; coagulation factor Xla inhibitor; proteinase nexin II (PN-II)
 V/Contains: amyloid beta protein long, plaque form; amyloid beta protein short, vascular form; amyloid beta protein precursor splice form APP(695); amyloid protein precursor splice form APP(751); amyloid protein precursor splice form APP(770)
 C/Species: Homo sapiens (man)
 C/Date: 30-Jun-1987 #sequence_revision 28-Jul-1995 #text_change 15-Sep-2000
 C/Accession: S02260; S05194; A32277; A33260; A35486; I39452; I39453; I39454; A4017; A4017; A03134; A29030; A47584; S02638; S00707; S00925; A38949; A30320; B30320; C30320; A31087; A24668; A28583; A29302; A60805; JL0038;

A:Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-770 <YOS1>
 A:Cross-references: GB:M33112; NID:gl78613; PIDN:AAB59502.1; PID:gl78616
 A:Accession: 139451
 A:Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-530, 'QWLMPVAFWEAKVGR' <YOS2>
 A:Cross-references: GB:M34875; NID:gl78608; PIDN:AAB59501.1; PID:gl78615
 R:Yoshikai, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sakaki, Y.
 Gene 102, 291-292, 1991
 A:Reference number: A59020; MUID:91340168; PMID:1908403
 A:Contents: annotation; erratum
 A>Note: revised physical map for reference 139451
 R:Levy, E.; Carman, M.D.; Fernandez-Madrid, I.J.; Power, M.D.; Lieberburg, I.; van Duinen, S.G.; Betts, G.T.; Luyendijk, W.; Frangione, B.
 Science 248, 1124-1126, 1990
 A:Title: Mutation of the Alzheimer's disease amyloid gene in hereditary cerebral hemorrhage, Dutch type.
 A:Reference number: 139453; MUID:90260663; PMID:2111584
 A:Accession: 139453
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 656-737 <LEV>
 A:Cross-references: GB:M37896; NID:gl78618; PIDN:AAA51727.1; PID:gl78620
 A>Note: a mutation with 693-Gln is presented
 R:Murrell, J.; Farlow, M.; Ghetii, B.; Benson, M.D.
 Science 254, 97-99, 1991
 A:Title: A mutation in the amyloid precursor protein associated with hereditary Alzheimer's disease.
 A:Reference number: 159462; MUID:92022553; PMID:1925564
 A:Accession: 159562
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 689-716, 'P' 718-737 <MUR>
 A:Cross-references: GB:S57665; NID:g236720; PIDN:AAB19991.1; PID:g236721
 R:Kamino, K.; Orr, H.T.; Payami, H.; Wilmsman, E.M.; Alonso, M.E.; Pulst, S.M.; Anderson, L.; O'dahl, S.; Nemens, E.; White, J.A.; Sadovnick, A.D.; Ball, M.J.; Kaye, J.; Warren, A.; McInnis, M.; Antonarakis, S.E.; Korenberg, J.R.; Sharma, V.; Kukull, W.; Larson, E.; Heston, L.L.; Martin, G.M.; Bird, T.D.; Schellenberg, G.D.
 Am. J. Hum. Genet. 51, 998-1014, 1992
 A:Title: Linkage and mutational analysis of familial Alzheimer disease kindreds for the APP gene region.
 A:Reference number: A44017; MUID:93035397; PMID:1415269
 A:Accession: A44017
 A:Molecule type: DNA
 A:Residues: 687-692, 'G' 694-718 <KAM>
 A:Cross-references: GB:S45133; NID:g257377; PIDN:AAB23645.1; PID:g257378
 A:Experimental source: familial Alzheimer disease family SB
 A>Note: sequence extracted from NCI backbone (NCBIP:115374)
 A:Accession: B44017
 A:Molecule type: DNA
 A:Residues: 687-718 <KAM2>
 A:Cross-references: GB:S45136; NID:g257379; PIDN:AAB23646.1; PID:g257380

A:Experimental source: familial Alzheimer disease family LIT
 A>Note: sequence extracted from NCI backbone (NCBIP:115376)
 A>Note: this sequence has a silent mutation
 R:Kang, J.; Lemaire, H.G.; Unterbeck, A.; Salbaum, J.M.; Masters, C.L.; Grzeschik, K.H.; Multhaup, G.; Beyreuther, K.; Muller-Hill, B.
 Nature 325, 733-736, 1987
 A:Title: The precursor of Alzheimer's disease amyloid A4 protein resembles a cell-surface receptor.
 A:Reference number: A03134; MUID:87144572; PMID:2881207
 A:Accession: A03134
 A:Molecule type: mRNA
 A:Residues: 1-288, 'V' 365-770 <KAN>
 A:Cross-references: GB:I00264; NID:g28525; PIDN:CAA68374.1; PID:g28526
 R:Robakis, N.K.; Ramakrishna, N.; Wolfe, G.; Wisniewski, H.M.
 Proc. Natl. Acad. Sci. U.S.A. 84, 4190-4194, 1987
 A:Title: Molecular cloning and characterization of a cDNA encoding the cerebrovascular and the neuritic plaque amyloid peptides.
 A:Reference number: A29030; MUID:87231971; PMID:3035574
 A:Accession: A29030
 A:Molecule type: mRNA
 A:Residues: 284-288, 'V' 365-646, 'E' 648-770 <ROB>
 A:Cross-references: GB:M16765; NID:gl78539; PIDN:AAA51722.1; PID:gl78540
 A>Note: the authors translated the codon GAG for residue 647 as Asp
 R:Goldgaber, D.; Lerman, M.I.; McBride, O.W.; Saffiotti, U.; Gajdusek, D.C.
 Science 235, 877-880, 1987
 A:Title: Characterization and chromosomal localization of a cDNA encoding brain amyloid of Alzheimer's disease.
 A:Reference number: A47584; MUID:87120328; PMID:3810169
 A:Accession: A47584
 A:Molecule type: mRNA
 A:Residues: 674-756, 'S' 758-770 <GOL>
 A:Cross-references: GB:M15533; NID:gl78706; PIDN:AAA35540.1; PID:gl78707
 R:Tanzi, R.E.; Gusella, J.F.; Watkins, P.C.; Bruns, G.A.P.; St George-Hyslop, P.; Van Keuren, M.L.; Patterson, D.; Pagan, S.; Kurnit, D.M.; Neve, R.L.
 Science 235, 880-884, 1987
 A:Title: Amyloid beta protein gene: cDNA, mRNA distribution, and genetic linkage near the Alzheimer locus.
 A:Reference number: A47585; MUID:87120329; PMID:2949367
 A:Accession: A47585
 A:Molecule type: mRNA
 A:Residues: 674-703 <TAN1>
 A:Cross-references: GB:M15532; NID:gl77957; PIDN:AAA51564.1; PID:gl77958
 R:Dyrks, T.; Weidemann, A.; Multhaup, G.; Salbaum, J.M.; Lemaire, H.G.; Kang, J.; Mueller-Hill, B.; Masters, C.L.; Beyreuther, K.
 EMBO J. 7, 949-957, 1988
 A:Title: Identification, transmembrane orientation and biogenesis of the amyloid A4 precursor of Alzheimer's disease.
 A:Reference number: S02638; MUID:86296437; PMID:2900137
 A:Accession: S02638
 A:Molecule type: mRNA
 A:Residues: 672-678 <DYR>
 R:Tanzi, R.E.; McClatchey, A.I.; Lamperti, E.D.; Villa-Komaroff, L.; Gusella, J.F.; Neve, R.L.
 Nature 331, 528-530, 1988

A/Title: Protease inhibitor domain encoded by an amyloid protein precursor mRNA associated with Alzheimer's disease.
A/Reference number: S00707; PMID:86122640; PMID:2693290
A/Accession: S00707
A/Molecule type: mRNA
A/Residues: 286-344, '1', 365-366 <TAN2>
A/Status: not compared with conceptual translation
A/Cross-references: EMBL:X06992; NID:g28817; PID:CAA30042.1; PID:g29612
A/Experimental source: promyelocytic leukemia cell line HL60
A/Note: alternative splice form APP(751)
R/Ponte, P.; Gonzalez-Dewhitt, P.; Schilling, J.; Miller, J.; Hsu, D.; Greenberg, B.; Davis, K.; Wallace, W.; Lieberburg, I.; Fuller, F.; Cordell, B.
Nature 331, 525-527, 1988
A/Title: A new A4 amyloid mRNA contains a domain homologous to serine proteinase inhibitors.
A/Reference number: S00925; PMID:86122639; PMID:2693289
A/Accession: S00925
A/Molecule type: mRNA
A/Residues: 1-344, '1', 365-770 <PO2>
A/Cross-references: GB:X06989; EMBL:Y00297; NID:g28720; PID:CAA30050.1; PID:g28721
A/Status: not compared with conceptual translation
R/Kataguchi, N.; Takahashi, Y.; Tokushima, Y.; Shiojiri, S.; Ito, H.
Nature 331, 530-532, 1988
A/Title: Novel precursor of Alzheimer's disease amyloid protein shows protease inhibitory activity.
A/Reference number: A38949; PMID:86122641; PMID:2693291
A/Accession: A38949
A/Molecule type: mRNA
A/Residues: 287-367 <KIT>
A/Cross-references: GB:X06991; NID:g28816; PID:CAA30041.1; PID:g29611
A/Experimental source: glioblastoma cell line
A/Note: alternative splice form APP(770)
R/Vitek, M.P.; Rasool, C.G.; de Sauvage, F.; Vitek, S.M.; Bartus, R.T.; Beer, B.; Ashton, R.A.; Macq, A.F.; Maloteaux, J.M.; Blume, A.J.; Octave, J.N.
Brain Res. Mol. Brain Res. 4, 121-131, 1988
A/Title: Absence of mutation in the beta-amyloid cDNAs cloned from the brains of three patients with sporadic Alzheimer's disease.
A/Reference number: A30320
A/Accession: A30320
A/Status: not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 284-288, '1', 365-770 <VIT1>
A/Accession: B30320
A/Status: not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 122-288, '1', 365-770 <VIT2>
A/Accession: C30320
A/Status: not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 606-770 <VIT3>
R/Zain, S.B.; Salim, M.; Chou, W.G.; Sajdel-Sulkowska, E.M.; Majocha, R.E.; Marotta, C.A.
Proc. Natl. Acad. Sci. U.S.A. 85, 929-933, 1988
A/Title: Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer disease brain: coding and noncoding regions of the fetal precursor mRNA are expressed in the cortex.
A/Reference number: A31087; PMID:86124954; PMID:2693379

A/Accession: A31087
A/Molecule type: mRNA
A/Residues: 507-770 <2AI>
A/Cross-references: GB:M18734; NID:g178572; PID:AAA51726.1; PID:g178573
A/Note: the authors translated the codon GAA for residue 599 as Gly, ACC for residue 603 as Val, GGC for residue 604 as Glu, GAG for residue 605 as Leu, CTT for residue 607 as Pro, CCC for residue 608 as Val, GGC for residue 609 as Asn, AAT for residue 610 as Gly, and GGT for residue 655 as Ser
A/Note: the cited Genbank accession number, J03594, is not in release 101.0
R/Masters, C.L.; Multhaup, G.; Simms, G.; Pottgiesser, J.; Martins, R.N.; Beyreuther, K.
Query Match 100.0%; Score 57; DB 1; Length 770;
Best Local Similarity 100.0%; Pred. No. 0.01; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0;
QY 1 KKQYTSIHGG 10
|||||
Db 725 KKQYTSIHGG 734
|||||
RESULT 6
JH0773
Alzheimer's disease amyloid beta protein precursor - African clawed frog
C/Species: Xenopus laevis (African clawed frog)
C/Date: 10-Jun-1993 #sequence_revision 10-Jun-1993 #text_change 13-Aug-1999
C/Accession: JH0773
R/Okado, H.; Okamoto, H.
Biochem. Biophys. Res. Commun. 189, 1561-1568, 1992
A/Title: A Xenopus homologue of the human beta-amyloid precursor protein: developmental regulation of its gene expression.
A/Reference number: JH0773; PMID:93129227; PMID:1282805
A/Accession: JH0773
A/Molecule type: mRNA
A/Residues: 1-747 <OKA>
A/Cross-references: GB:S52417; NID:g263150; PID:AA24853.1; PID:g263151
A/Experimental source: larva
C/Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase inhibitor homology
C/Keywords: alternative splicing; amyloid
F:287-337/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
Query Match 94.7%; Score 54; DB 2; Length 747;
Best Local Similarity 90.0%; Pred. No. 0.036; Indels 0; Gaps 0;
Matches 9; Conservative 1; Mismatches 0;
QY 1 KKQYTSIHGG 10
|||||
Db 702 KKQYTSIHGG 711
|||||
Search completed: October 4, 2004, 18:58:23
Job time : 14.7826 secs

OM protein - protein search, using sw model

Run on: October 4, 2004, 18:44:39 ; Search time 8.26087 Seconds
(without alignments)
63.032 Million cell updates/sec

Title: US-10-048-203-3
Perfect score: 57
Sequence: 1 KKQYTSIHG 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues
Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	57	100.0	737	1 A4_FUGRU	Q93279 fugu rubrip
2	57	100.0	731	1 A4_SAISC	Q95241 s amyloid b
3	57	100.0	770	1 A4_CAVPO	Q60495 c amyloid b
4	57	100.0	770	1 A4_HUMAN	P05067 h amyloid b
5	57	100.0	770	1 A4_MACFA	P53601 m amyloid b
6	57	100.0	770	1 A4_MOUSE	P12023 m amyloid b
7	57	100.0	770	1 A4_PIG	P79307 s amyloid b
8	57	100.0	770	1 A4_RAT	P08592 r amyloid b
9	57	100.0	780	1 A4_TETEL	Q73683 tetradodon f
10	39	68.4	452	1 NU4M_LUMTE	Q34949 lumbricus t
11	38	66.7	379	1 ISPH_SYNY3	Q55643 synchocyst
12	38	66.7	458	1 YGM9_YEAST	Q01163 saccharomyc
13	37	64.9	142	1 Y4KQ_RHISN	P55535 rhizobium s
14	36	63.2	659	1 CYOB_BUCAP	Q8K994 buchnera ap
15	36	63.2	1268	1 YAD6_CAEEL	Q09575 caenorhabdi
16	35	61.4	197	1 PSD9_CAEEL	Q10920 caenorhabdi
17	35	61.4	443	1 GAT3_HUMAN	P23771 homo sapien

18	35	61.4	443	1 GAT3_MOUSE	P23772 mus musculu
19	35	61.4	695	1 APP2_MOUSE	Q06335 mus musculu
20	35	61.4	739	1 PURL_LISIN	Q92an9 listeria in
21	35	61.4	739	1 PURL_LISMO	Q8Y6c1 listeria mo
22	35	61.4	753	1 CAT2_NEUCR	Q8X182 neurospora
23	35	61.4	763	1 APP2_HUMAN	Q06481 homo sapien
24	35	61.4	763	1 APP2_RAT	P13943 rattus norv
25	34	59.6	348	1 NTRB_PROVU	P28788 proteus vul
26	34	59.6	366	1 TF3A_XENLA	P03001 xenopus lae
27	34	59.6	660	1 VNCS_PAVPN	P18547 porcine par
28	34	59.6	662	1 VNCS_PAVPK	P52502 porcine par
29	34	59.6	782	1 MUS2_STAEP	Q8ep16 staphylococ
30	34	59.6	1406	1 TOP1_CANGA	Q93794 candida gla
31	33	57.9	82	1 BOP_EPPL	P22499 bacteriopia
32	33	57.9	117	1 HEMJ_LINON	P22765 lingula ung
33	33	57.9	157	1 SSRP_CHLTE	Q8Kw48 chlorobium
34	33	57.9	177	1 RELX_MESAU	Q64171 mesocricetu
35	33	57.9	249	1 CREB_CHLYR	P51984 chlorochydr
36	33	57.9	326	1 2N73_HUMAN	Q43830 homo sapien
37	33	57.9	329	1 TF3A_XENBO	P17842 xenopus bor
38	33	57.9	361	1 SERC_BACHD	Q9Kdm4 bacillus ha
39	33	57.9	412	1 REA_CAEEL	P90917 caenorhabdi
40	33	57.9	519	1 LEU1_CANEF	Q7vdj6 candidatus
41	33	57.9	530	1 UDEC_RAT	P36311 rattus norv
42	33	57.9	530	1 UDEC_RABIT	P36313 oryctolagus
43	33	57.9	580	1 SYD_MYCPE	Q8wb7 mycoplasma
44	33	57.9	645	1 ACS2_PSEAE	Q9hv66 pseudomonas
45	33	57.9	683	1 CV19_HUMAN	Q13769 homo sapien

ALIGNMENTS

RESULT 1				
A4_FUGRU				
ID A4_FUGRU	STANDARD;	PRT;	737 AA.	
AC Q93279;				
DT 10-OCT-2003 (Rel. 42, Created)				
DT 10-OCT-2003 (Rel. 42, Last sequence update)				
DT 10-OCT-2003 (Rel. 42, Last annotation update)				
DE Alzheimer's disease amyloid A4 protein homolog precursor [Contains:				
DE Beta-amyloid protein (Beta-APP) (A-beta)].				
GN APP.				
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).				
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;				
OC Acanthomorpha; Acanthopterygii; Percomorphi; Tetraodontiformes;				
OC Tetraodontoidea; Tetraodontidae; Takifugu.				
OX NCBI_TaxID=31033;				
RN [1]				
RP SEQUENCE FROM N.A.				
RX MEDLINE=98252138; PubMed=9599080;				
RA Villard L., Tassone F., Crnogorac-Jurcovic T., Clancy K., Gardiner K.;				
RT "Analysis of pufferfish homologues of the AT-rich human APP gene.";				
RL Gene 210:17-24(1998).				
CC - - FUNCTION: Functional neuronal receptor which couples to				
CC intracellular signaling pathway through the GTP-binding protein				

CC G(O) (By similarity).

CC -|- SUBCELLULAR LOCATION: Type I membrane protein.

CC -|- SIMILARITY: Belongs to the APP family.

CC -|- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.

CC -----

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CC or send an email to license@isb-sib.ch).

CC -----

DR EML; AF090120; AAD13392.1; -.

DR HSSP; P05067; 1HZ3.

DR InterPro; IPR008155; A4_APP.

DR InterPro; IPR008154; A4_EXTRA.

DR InterPro; IPR001255; Beta_APP.

DR InterPro; IPR002223; Kunitz_BPTI.

DR Pfam; PF02177; A4_EXTRA; 1.

DR Pfam; PF03494; Beta_APP; 1.

DR Pfam; PF00014; Kunitz_BPTI; 1.

DR PRINTS; PRO0203; AMYLOIDA4.

DR PRINTS; PRO0759; BASICPASE.

DR ProDom; PD000222; Kunitz_BPTI; 1.

DR SMART; SMO0065; A4_EXTRA; 1.

DR SMART; SMO0131; KUT; 1.

DR PROSITE; PS00319; A4_EXTRA; FALSE_NEG.

DR PROSITE; PS00320; A4_INTRA; 1.

DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.

DR PROSITE; PS00279; BPTI_KUNITZ_2; 1.

KW Glycoprotein; Amyloid; Neurone; Transmembrane; Signal;

KW Serine protease inhibitor.

FT SIGNAL 1 18 POTENTIAL.

FT CHAIN 19 737 ALZHEIMER'S DISEASE AMYLOID A4

FT PROTEIN HOMOLOG.

FT CHAIN 639 681 BETA-AMYLOID PROTEIN (POTENTIAL).

FT DOMAIN 19 668 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 669 689 POTENTIAL.

FT DOMAIN 690 737 CYTOPLASMIC (POTENTIAL).

FT DOMAIN 286 344 BPTI/KUNITZ INHIBITOR.

FT SITE 726 729 CLATHRIN-BINDING (BY SIMILARITY).

FT ACT_SITE 300 301 REACTIVE BOND.

FT DISULFID 290 340 BY SIMILARITY.

FT DISULFID 299 323 BY SIMILARITY.

FT DISULFID 315 336 BY SIMILARITY.

FT CARBOHYD 522 522 N-LINKED (GLCNAC...) (POTENTIAL).

SQ SEQUENCE 737 AA; 82856 MW; 6FAD01E253B2B7E2 CRC64;

Query Match 100.0%; Score 57; DB 1; Length 737;

Best Local Similarity 100.0%; Pred. No. 0.0025;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKYQTSIHGG 10

DB 692 KKYQTSIHGG 701

RESULT 2

A4_SAISC STANDARD; PRT; 751 AA.

ID A4_SAISC Q95241;

AC 15-DEC-1998 (Rel. 37, Created)

DT 15-DEC-1998 (Rel. 37, Last sequence update)

DR 10-OCT-2003 (Rel. 42, Last annotation update)

DE Amyloid beta A4 protein precursor (APP) (Alzheimer's disease amyloid

DE protein homolog) [Contains: Soluble APP-alpha (S-APP-alpha); Soluble

DE APP-beta (S-APP-beta); C99; Beta-amyloid protein 42 (Beta-APP42);

DE Beta-amyloid protein 40 (Beta-APP40); C83; P3(42); P3(40); Gamma-

DE CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-CTF(57)

DE (Gamma-secretase C-terminal fragment 57); Gamma-CTF(50) (Gamma-

DE secretase C-terminal fragment 50); C31].

GN APP.

OS Saimiri sciureus (Common squirrel monkey).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Saimiri.

OX NCBI_TaxID=9521;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Kidney, and Liver;

RX MEDLINE=96108492; PubMed=8332114;

RA Levy E., Amorim A., Frangione B., Walker L.C.;

RT "Beta-amyloid precursor protein gene in squirrel monkeys with

RT cerebral amyloid angiopathy."

RL Neurobiol. Aging 16:805-808(1995).

-|- FUNCTION: Functions as a cell surface receptor and performs

physiological functions on the surface of neurons relevant to

neurite growth, neuronal adhesion and axonogenesis. Involved in

cell mobility and transcription regulation through protein-protein

interactions (By similarity). Can promote transcription activation

through binding to APBB1/Tip60 and inhibit Notch signaling through

interaction with Numb (By similarity). Couples to apoptosis-

inducing pathways such as those mediated by G(O) and JIP (By

similarity). Inhibits G(O) alpha Affase activity (By similarity).

Acts as a kinesin I membrane receptor, mediating the axonal

transport of beta-secretase and presenilin 1 (By similarity). May

be involved in copper homeostasis/oxidative stress through copper

ion reduction. In vitro, copper-metalated APP induces neuronal

death directly or is potentiated through Cu(II)-mediated low-

density lipoprotein oxidation (By similarity). Can regulate

neurite outgrowth through binding to components of the

extracellular matrix such as heparin and collagen I and IV (By

similarity). The splice isoforms that contain the BPTI domain

possess protease inhibitor activity (By similarity).

-|- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators

with metal-reducing activity. Bind transient metals such as

copper, zinc and iron (By similarity).

-|- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved

peptides, including C31, are potent enhancers of neuronal

apoptosis (By similarity).

-|- SUBUNIT: Binds, via its C-terminal, to the PID domain of several

cytoplasmic proteins, including APBB family members, the APEA

family, MAPK8IP1, and SHC1, Numb and Dab1 (By similarity). Binding

to Dab1 inhibits its serine phosphorylation (By similarity). Also

interacts with GPCR-like protein BP2, FPR1, APPBP1, IBL, KMS2 (via its TPR domains) (By similarity), APPBP2 (via BASS) and DBP1. In vitro, it binds MAPT via the MT-binding domains (By similarity). Associates with microtubules in the presence of ATP and in a kinase-dependent manner (By similarity).

SUBCELLULAR LOCATION: Type I membrane protein. Cell surface protein that rapidly becomes internalized via clathrin-coated pits. During maturation, the immature APP (N-glycosylated in the endoplasmic reticulum) moves to the Golgi complex where complete maturation occurs (O-glycosylated and sulfated). After alpha-secretase cleavage, soluble APP is released into the extracellular space and the C-terminal is internalized to endosomes and lysosomes. Some APP accumulates in secretory transport vesicles leaving the late Golgi compartment and returns to the cell surface. Gamma-CTF(59) peptide is located to both the cytoplasm and nuclei of neurons (By similarity).

ALTERNATIVE PRODUCTS:

Event=Alternative splicing; Named isoforms=2;
Comment=Additional isoforms seem to exist;
Name=APP770;
IsoId=Q95241-1; Sequence=Displayed;
Name=APP695;
IsoId=Q95241-2; Sequence=Not described;

DOMAIN: The basolateral sorting signal (BASS) is required for sorting of membrane proteins to the basolateral surface of epithelial cells (By similarity).

DOMAIN: The NPXY sequence motif found in many tyrosine-phosphorylated proteins is required for the specific binding of the PID domain. However additional amino acids either N- or C-terminal to the NPXY motif are often required for complete interaction. The PID domain-containing proteins which bind APP require the YENPTY motif for full interaction. These interactions are independent of phosphorylation on the terminal tyrosine residue. The NPXY site is also involved in clathrin-mediated endocytosis (By similarity).

PTM: Proteolytically processed under normal cellular conditions. Cleavage by alpha-secretase or alternatively by beta-secretase leads to generation and extracellular release of soluble APP peptides, S-APP-alpha and S-APP-beta, respectively, and the retention of corresponding membrane-anchored C-terminal fragments, C83 and C99. Subsequent processing of C83 by gamma-secretase yields P3 peptides. This is the major secretory pathway and is nonamyloidogenic. Alternatively, presenilin/nicastrin-mediated gamma-secretase processing of C99 releases the amyloid beta proteins, amyloid-beta 40 (Abeta40) and amyloid-beta 42 (Abeta42), major components of amyloid plaques, and the cytotoxic C-terminal fragments, gamma-CTF(50), gamma-CTF(57) and gamma-CTF(59) (By similarity).

PTM: Proteolytically cleaved by caspases during neuronal apoptosis (By similarity). Cleavage at Asp-720 by either caspase-3, -8 or -9 results in the production of the neurotoxic C31 peptide and the increased production of beta-amyloid peptides (By similarity).

PTM: N- and O-glycosylated (By similarity).

PTM: Phosphorylation in the C-terminal on tyrosine, threonine and serine residues is neuron-specific. Phosphorylation can affect APP processing, neuronal differentiation and interaction with other proteins (By similarity).

MISCELLANEOUS: Chelation of metal ions, notably copper, iron and zinc, can induce histidine-bridging between beta-amyloid molecules resulting in beta-amyloid-metal aggregates (By similarity). Extracellular zinc-binding increases binding of heparin to APP and inhibits collagen-binding (By similarity).

SIMILARITY: Belongs to the APP family.

SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.

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EMBL; S81024; A014347.1; -.
HSSP; P05067; IAAP.
InterPro; IPR008155; A4_APP.
InterPro; IPR008154; A4_extra.
InterPro; IPR001255; Beta-APP.
InterPro; IPR002223; Kunitz_BPTI.
Pfam; PF02177; A4_EXTRA; 1.
Pfam; PF03494; Beta-APP; 1.
Pfam; PF00014; Kunitz_BPTI; 1.
PRINTS; PR00203; AMYLOIDA4.
PRINTS; PR00759; BASICPTASE.
ProDom; PD000222; Kunitz_BPTI; 1.
SMART; SMO0006; A4_EXTRA; 1.
SMART; SMO0131; KU; 1.
PROSITE; PS00319; A4_EXTRA; 1.
PROSITE; PS00320; A4_INTRA; 1.
PROSITE; PS00280; BPTI_KUNITZ_1; 1.
PROSITE; PS00279; BPTI_KUNITZ_2; 1.
Apoptosis; Endocytosis; Cell adhesion; Serine protease inhibitor; Coated pits; Neutone; Heparin-binding; Metal-binding; Copper; Iron; Zinc; Signal; Transmembrane; Glycoprotein; Phosphorylation; Proteoglycan; Amyloid; Alternative splicing.
FT SIGNAL 1 17 BY SIMILARITY.
FT CHAIN 18 751 A4 PROTEIN.
FT CHAIN 18 668 SOLUBLE APP-ALPHA (POTENTIAL).
FT CHAIN 18 652 SOLUBLE APP-BETA (POTENTIAL).
FT CHAIN 653 751 C99 (POTENTIAL).
FT CHAIN 653 694 BETA-AMYLOID PROTEIN 42 (POTENTIAL).
FT CHAIN 653 692 BETA-AMYLOID PROTEIN 40 (POTENTIAL).
FT CHAIN 669 751 C83 (POTENTIAL).
FT CHAIN 669 694 P3(42) (POTENTIAL).
FT CHAIN 669 692 P3(40) (POTENTIAL).
FT CHAIN 693 751 GAMMA-CTF(59) (POTENTIAL).
FT CHAIN 695 751 GAMMA-CTF(57) (POTENTIAL).
FT CHAIN 702 751 GAMMA-CTF(50) (POTENTIAL).
FT CHAIN 721 751 C31 (POTENTIAL).
FT CHAIN 721 680 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 18 704 POTENTIAL.
FT TRANSMEM 681 704 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 705 751 HEPARIN-BINDING (BY SIMILARITY).
FT DOMAIN 96 110 ZINC-BINDING (BY SIMILARITY).
FT DOMAIN 181 188

FT DOMAIN 291 341 BPTI/KNITZ INHIBITOR.
 FT DOMAIN 316 344 HEPARIN-BINDING (BY SIMILARITY).
 FT DOMAIN 363 428 HEPARIN-BINDING (BY SIMILARITY).
 FT DOMAIN 504 521 COLLAGEN-BINDING (BY SIMILARITY).
 FT DOMAIN 713 732 INTERACTION WITH G(O)-ALPHA
 (BY SIMILARITY).
 FT DOMAIN 230 260 ASP/GLU-RICH (ACIDIC).
 FT DOMAIN 274 280 POLY-THR.
 FT SITE 144 144 REQUIRED FOR COPPER(II) REDUCTION
 (BY SIMILARITY).
 FT ACT_SITE 301 302 REACTIVE BOND.
 FT SITE 652 653 CLEAVAGE (BY BETA-SECRETASE)
 (BY SIMILARITY).
 FT SITE 653 654 CLEAVAGE (BY CASPASE-6) (BY SIMILARITY).
 FT SITE 668 669 CLEAVAGE (BY ALPHA-SECRETASE)
 (BY SIMILARITY).
 FT SITE 685 685 INVOLVED IN FREE RADICAL PROPAGATION
 (BY SIMILARITY).
 FT SITE 687 687 INVOLVED IN OXIDATIVE REACTIONS
 (BY SIMILARITY).
 FT SITE 692 693 CLEAVAGE (BY GAMMA-SECRETASE; SITE 1)
 (BY SIMILARITY).
 FT SITE 694 695 CLEAVAGE (BY GAMMA-SECRETASE; SITE 2)
 (BY SIMILARITY).
 FT SITE 701 702 CLEAVAGE (BY GAMMA-SECRETASE; SITE 3)
 (BY SIMILARITY).
 FT SITE 705 715 BASOLATERAL SORTING SIGNAL
 (BY SIMILARITY).
 FT SITE 720 721 CLEAVAGE (BY CASPASES-3,-6,-8 OR -9)
 (BY SIMILARITY).
 FT SITE 738 741 ENDOCYTOSIS SIGNAL.
 FT SITE 740 743 NPXY MOTIF.

Query Match 100.0%; Score 57; DB 1; Length 751;
 Best Local Similarity 100.0%; Pred. No. 0.0026;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KQQYTSIHG 10
 |||||
 Db 706 KQQYTSIHG 715

RESULT 3
 A4_CAVPO STANDARD; PRT; 770 AA.
 AC Q60495; Q60496;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DE Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
 amyloid protein homolog) [Contains: Soluble APP-alpha (S-APP-alpha);
 Soluble APP-beta (S-APP-beta); CTF-alpha; CTF-beta; Beta-amyloid
 protein 42 (Beta-APP42); Beta-amyloid protein 40 (Beta-APP40); P3(42);
 P3(40); CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-
 CTF(57) (Gamma-secretase C-terminal fragment 57); C31].
 GN APP.
 OS Cavia porcellus (Guinea pig).

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
 CC NCBI_taxid=10141;
 CC [1]
 CC SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
 CC TISSUE=Brain, and Liver;
 CC MEDLINE=97236426; PubMed=9116031;
 CC Beck M., Mueller D., Bigl V.;
 CC "Amyloid precursor protein in Guinea pigs - complete cDNA sequence and
 CC alternative splicing.";
 CC Biochim. Biophys. Acta 1351:17-21(1997).
 CC [2]
 CC INTERACTION OF BETA-APP40 WITH APOE.
 CC MEDLINE=98007700; PubMed=9349544;
 CC Martel C.L., Mackic J.B., Matsubara E., Governale S., Miguel C.,
 CC Miao W., McComb J.G., Frangione B., Ghiso J., Zlokovic B.V.;
 CC "Isoform-specific effects of apolipoproteins E2, E3, and E4 on
 CC cerebral capillary sequestration and blood-brain barrier transport of
 CC circulating Alzheimer's amyloid beta.";
 CC J. Neurochem. 69:1995-2004(1997).
 CC [3]
 CC PROCESSING.
 CC MEDLINE=20084499; PubMed=10619481;
 CC Beck M., Brueckner M.K., Holzer M., Kaap S., Pannicke T., Arendt T.,
 CC Bigl V.;
 CC "Guinea-pig primary cell cultures provide a model to study expression
 CC and amyloidogenic processing of endogenous amyloid precursor
 CC protein.";
 CC Neurosci. 95:243-254(2000).
 CC [4]
 CC GAMMA-SECRETASE PROCESSING.
 CC MEDLINE=20576391; PubMed=11035007;
 CC Pinnix I., Muanuru U., Tun H., Sridharan A., Golde T., Eckman C.,
 CC Ziani-Cherif C., Onstead L., Sambamurti K.;
 CC "A novel gamma -secretase assay based on detection of the putative
 CC C-terminal fragment-gamma of amyloid beta protein precursor.";
 CC J. Biol. Chem. 276:481-487(2001).
 CC -1- FUNCTION: Functions as a cell surface receptor and performs
 CC physiological functions on the surface of neurons relevant to
 CC neurite growth, neuronal adhesion and axonogenesis. Involved in
 CC cell mobility and transcription regulation through protein-protein
 CC interactions (By similarity). Can promote transcription activation
 CC through binding to APBB1/Tip60 and inhibit Notch signaling through
 CC interaction with Numb (By similarity). Couples to apoptosis-
 CC inducing pathways such as those mediated by G(O) and JIP (By
 CC similarity). Inhibits G(O) alpha Affase activity (By similarity).
 CC Acts as a kinesin I membrane receptor, mediating the axonal
 CC transport of beta-secretase and presenilin 1 (By similarity). May
 CC be involved in copper homeostasis/oxidative stress through copper
 CC ion reduction (By similarity). In vitro, copper-metallated APP
 CC induces neuronal death directly or is potentiated through Cu(II)-
 CC mediated low-density lipoprotein oxidation (By similarity). Can
 CC regulate neurite outgrowth through binding to components of the
 CC extracellular matrix such as heparin and collagen I and IV (By
 CC similarity). The splice isoforms that contain the BPTI domain
 CC possess protease inhibitor activity (By similarity).
 CC -1- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators

with metal-reducing activity. Bind transient metals such as copper, zinc and iron. Beta-amyloid peptides bind to lipoproteins and apolipoproteins E and J in the CSF and to HDL particles in plasma, inhibiting metal-catalyzed oxidation of lipoproteins.

-!- FUNCTION: Apolipoproteins elicit adhesion of neural cells to the extracellular matrix and may regulate neurite outgrowth in the brain (By similarity).

-!- FUNCTION: The gamma-CRF peptides as well as the caspase-cleaved peptides, including Cbl, are potent enhancers of neuronal apoptosis (By similarity).

-!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several cytoplasmic proteins, including APBB family members, the APBA family, MAPKIP1, SHC1 and Numb and Dab1 (By similarity). Also interacts with GPCR-like protein BPP, FPR1, APBP1, IBI, KNS2 (via its TPR domain), APBP2 (via BASS) and DBI (By similarity). Associates with microtubules in the presence of ATP and in a kinesin-dependent manner (By similarity). Soluble Abeta40 binds all three isoforms of APOE, in vitro and in vivo. When lipidated, APOE3 appears to be the preferred amyloid binding isoform, while the apoE4 isoform-beta-APO40 complex is capable of being transported across the blood-brain barrier.

-!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface protein that rapidly becomes internalized via clathrin-coated pits (By similarity). During maturation, the immature APP (N-glycosylated in the endoplasmic reticulum) moves to the Golgi complex where complete maturation occurs (O-glycosylated and sulfated) (By similarity). After alpha-secretase cleavage, soluble APP is released into the extracellular space and the C-terminal is internalized to endosomes and lysosomes (By similarity). Some APP accumulates in secretory transport vesicles leaving the late Golgi compartment and returns to the cell surface (By similarity). APP sorts to the basolateral surface in epithelial cells (By similarity).

-!- ALTERNATIVE PRODUCTS:

Event=Alternative splicing; Named isoforms=2;

Comment=Additional isoforms, missing exons 7,8 and 15, seem to exist. The L-isoforms, missing exon 15, are referred to as appicans;

Name=APP770;

IsoId=Q60495-1; Sequence=Displayed;

Name=APP695;

IsoId=Q60495-2; Sequence=VSP_007221; VSP_007222;

IsoId=Q60495-3; Sequence=VSP_007223;

-!- TISSUE SPECIFICITY: Isoform APP695 is the major isoform found in brain. The longer isoforms containing the BPTI domain are predominantly expressed in peripheral organs such as muscle and liver.

-!- INDUCTION: Increased levels during neuronal differentiation.

-!- DOMAIN: The basolateral sorting signal (BASS) is required for sorting of membrane proteins to the basolateral surface of epithelial cells.

-!- DOMAIN: The NPXY sequence motif found in many tyrosine-phosphorylated proteins is required for the specific binding of the PID domain. However additional amino acids either N- or C-terminal to the NPXY motif are often required for complete interaction. The PID domain-containing proteins which bind APP require the YENPTY motif for full interaction. These interactions are independent of phosphorylation on the terminal tyrosine

residue (By similarity). The NPXY site is also involved in clathrin-mediated endocytosis.

-!- FM: Proteolytically processed under normal cellular conditions. Cleavage by alpha-secretase or alternatively by beta-secretase leads to generation and extracellular release of soluble APP peptides, S-APP-alpha and S-APP-beta, respectively, and the retention of corresponding membrane-anchored C-terminal fragments, CTF-alpha and CTF-beta. Subsequent processing of CTF-alpha by gamma-secretase yields P3 peptides. This is the major secretory pathway and is nonamyloidogenic. Alternatively, processing of CTF-presenilin/nicastrin-mediated gamma-secretase processing of CTF-beta releases the amyloid beta proteins, amyloid-beta 40 (Abeta40) and amyloid-beta 42 (Abeta42), major components of amyloid plaques, and the corresponding cytotoxic C-terminal fragments (CTFs).

-!- PTM: Proteolytically cleaved by caspase-3 during neuronal apoptosis (By similarity).

-!- PTM: N- and O-glycosylated. O-linkage of chondroitin sulfate to the L-APP isoforms produces the APP proteoglycan core proteins, the appicans (By similarity).

-!- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and serine residues is neuron-specific (By similarity). Phosphorylation can affect APP processing, neuronal differentiation and interaction with other proteins.

-!- PTM: Extracellular binding and reduction of copper, results in a corresponding oxidation of Cys-144 and Cys-159, and the formation of a disulfide bond (By similarity).

-!- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and zinc, can induce histidine-bridging between beta-amyloid molecules resulting in beta-amyloid-metal aggregates.

-!- SIMILARITY: Belongs to the APP family.

-!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.

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EMBL; X57631; CAA66230.1; -.

EMBL; X99198; CAA67599.1; -.

HSSP; P05067; 1BA4.

InterPro; IPR008155; A4_APP.

InterPro; IPR008154; A4_extra.

InterPro; IPR002223; Kunitz_BPTI.

Pfam; PF00014; Kunitz_BPTI; 1.

PRINTS; PR00203; AMYLOIDA4.

PRINTS; PR00759; BASICPTASE.

ProDom; PD000222; Kunitz_BPTI; 1.

SMART; SM00006; A4_EXTRA; 1.

SMART; SM00131; KU; 1.

PROSITE; PS00319; A4_EXTRA; 1.

PROSITE; PS00320; A4_INTRA; 1.

PROSITE; PS00280; BPTI_KUNITZ_1; 1.

PROSITE; PS00279; BPTI_KUNITZ_2; 1.

KW Apoptosis; Endocytosis; Cell adhesion; Serine protease inhibitor;
KW Coated pits; Neurone; Heparin-binding; Metal-binding; Copper; Iron;
KW Zinc; Signal; Transmembrane; Glycoprotein; Phosphorylation;
KW Proteoglycan; Alternative splicing; Amyloid.
FT SIGNAL 1 17 BY SIMILARITY.
FT CHAIN 18 770 AMYLOID BETA A4 PROTEIN.
FT CHAIN 18 697 SOLUBLE APP-ALPHA (BY SIMILARITY).
FT CHAIN 18 671 SOLUBLE APP-BETA (BY SIMILARITY).
FT CHAIN 672 770 CTF-ALPHA (BY SIMILARITY).
FT CHAIN 672 713 BETA-AMYLOID PROTEIN 42 (BY SIMILARITY).
FT CHAIN 672 711 BETA-AMYLOID PROTEIN 40 (BY SIMILARITY).
FT CHAIN 698 770 CTF-BETA (BY SIMILARITY).
FT CHAIN 698 713 P3(42) (BY SIMILARITY).
FT CHAIN 698 711 P3(40) (BY SIMILARITY).
FT CHAIN 712 770 GAMMA-CTF(59) (BY SIMILARITY).
FT CHAIN 714 770 GAMMA-CTF(57) (BY SIMILARITY).
Query Match 100.0%; Score 57; DB 1; Length 770;
Best Local Similarity 100.0%; Pred. No. 0.0027;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KKYQTSIHG 10
| | | | | | | | | |
Db 725 KKYQTSIHG 734
RESULT 4
A4_HUMAN
ID A4_HUMAN STANDARD; PRT; 770 AA.
AC P05067; P08000; P78438; Q13764; Q13778; Q13793; Q16011; Q16014;
AC Q16019; Q16020; Q9BT38; Q9UCA9; Q9UCB6; Q9UCB8; Q9UCD1; Q9UC58;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
DE amyloid protein) (Cerebral vascular amyloid peptide) (CVAP) (Protease
DE nexin-II) (PN-II) (APP1) (PRA4) [Contains: Soluble APP-alpha (S-APP-
DE alpha); Soluble APP-beta (S-APP-beta); C99; Beta-amyloid protein 42
DE (Beta-APP42); Beta-amyloid protein 40 (Beta-APP40); C83; P3(42);
DE P3(40); Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59)
DE (Amyloid intracellular domain 59) (AID(59)); Gamma-CTF(57) (Gamma-
DE secretase C-terminal fragment 57) (Amyloid intracellular domain 57)
DE (AID(57)); Gamma-CTF(50) (Gamma-secretase C-terminal fragment 50)
DE (Amyloid intracellular domain 50) (AID(50)); C31].
GN APP OR A4 OR AD1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM APP695).
RC TISSUE=Brain;
RX MEDLINE=87144572; PubMed=2881207;
RA Kang J., Lemaire H.-G., Unterbeck A., Salbaum J.M., Masters C.L.,
RA Grzeschik K.-H., Multhaup G., Beyreuther K., Mueller-Hill B.;
RT "The precursor of Alzheimer's disease amyloid A4 protein resembles a
RT cell-surface receptor.";
RL Eur. J. Neurosci. 18:102-108(2003).
RN [9]

RL Nature 325:733-736(1987).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM APP751).
RC TISSUE=Brain;
RX MEDLINE=88122639; PubMed=2893289;
RA Ponte P., Gonzalez-Dewhitt P., Schilling J., Miller J., Hau D.,
RA Greenberg B., Davis K., Wallace W., Lieberburg I., Fuller F.,
RA Cordell B.;
RT "A new A4 amyloid mRNA contains a domain homologous to serine
RT proteinase inhibitors.";
RL Nature 331:525-527(1988).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM APP695).
RX MEDLINE=89128427; PubMed=2783775;
RA Lemaire H.-G., Salbaum J.M., Multhaup G., Kang J., Bayney R.M.,
RA Unterbeck A., Beyreuther K., Mueller-Hill B.;
RT "The PRA4(695) precursor protein of Alzheimer's disease A4 amyloid
RT is encoded by 16 exons.";
RL Nucleic Acids Res. 17:517-522(1989).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM APP770).
RX MEDLINE=90236318; PubMed=2110105;
RA Yoshikai S.-I., Sasaki H., Doh-ura K., Furuya H., Sakaki Y.;
RT "Genomic organization of the human amyloid beta-protein precursor
RT gene.";
RL Gene 87:257-263(1990).
RN [5]
RP ERRATUM, AND REVISIONS.
RA Yoshikai S.-I., Sasaki H., Doh-ura K., Furuya H., Sakaki Y.;
RL Gene 102:291-292(1991).
RN [6]
RP SEQUENCE FROM N.A. (ISOFORM L-APP733).
RC TISSUE=Leukocyte;
RX MEDLINE=92268136; PubMed=1587857;
RA Koenig G., Moening U., Czech C., Prior R., Banati R.,
RA Schreier-Gasser U., Bauer J., Masters C.L., Beyreuther K.;
RT "Identification and differential expression of a novel alternative
RT splice isoform of the beta A4 amyloid precursor protein (APP) mRNA in
RT leukocytes and brain microglial cells.";
RL J. Biol. Chem. 267:10804-10809(1992).
RN [7]
RP SEQUENCE FROM N.A. (ISOFORM APP770).
RX MEDLINE=97263807; PubMed=9108164;
RA Hattori M., Tsukahara F., Furuhata Y., Tanahashi H., Hirose M.,
RA Saito M., Tsukuni S., Sakaki Y.;
RT "A novel method for making nested deletions and its application for
RT sequencing of a 300 kb region of human APP locus.";
RL Nucleic Acids Res. 25:1802-1808(1997).
RN [8]
RP SEQUENCE FROM N.A. (ISOFORM APP639).
RC TISSUE=Brain;
RX MEDLINE=22744650; PubMed=12859342;
RA Tang K., Wang C., Shen C., Shang S., Ravid R., Jing N.;
RT "Identification of a novel alternative splicing isoform of human
RT amyloid precursor protein gene, APP639.";
RL Eur. J. Neurosci. 18:102-108(2003).
RN [9]

RP SEQUENCE FROM N.A. (ISOFORM APP305).
RC TISSUE=Pancreas;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.D., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Pange C.,
RA Rosa S.S., McQuellan N.A., Peters G.J., Abramson R.D., Mullaney S.J.,
RA Bosak S.A., McManus P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Wozniak D., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallalón D.M., Mizny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Halton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blackley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smaluk D.E.,
RA Schermer A., Schell J.B., Jones S.J.M., Marra N.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16699-16903(2002).
RN [10]
RP SEQUENCE OF 1-10 FROM N.A.
RN
RP TISSUE=Liver;
RC MEDLINE=89016647; PubMed=3140222;
RX Schon E.A., Mita S., Sadlock J., Herbert J.;
RA "A cDNA specifying the human amyloid beta precursor protein (AβPP)
RT encodes a 95-kDa polypeptide.";
RL Nucleic Acids Res. 16:9351-9351(1988).
RN [11]
RP ERRATUM, AND REVISIONS.
RP Mita S., Sadlock J., Herbert J., Schon E.A.;
RN [12]
RN Nucleic Acids Res. 16:11402-11402(1988).
RP SEQUENCE OF 1-75 FROM N.A.
RX MEDLINE=89165870; PubMed=2538123;
RA LaFauci G., Lahiri D.K., Salton S.R., Robakis N.K.;
RT "Characterization of the 5'-end region and the first two exons of the
RT beta-protein precursor gene.";
RL Biochem. Biophys. Res. Commun. 159:297-304(1989).
RN [13]
RP SEQUENCE OF 18-50.
RC TISSUE=Fibroblast;
RX MEDLINE=87250462; PubMed=3597385;
RA van Nostrand W.E., Cunningham D.D.;
RT "Purification of protease nexin II from human fibroblasts.";
RL J. Biol. Chem. 262:8508-8514(1987).
RN [14]
RP PARTIAL SEQUENCE FROM N.A. (ISOFORM APP751).
RC TISSUE=Brain;
RX MEDLINE=89346754; PubMed=2569763;
RA de Sauvage F., Octave J.N.;
RT "A novel mRNA of the A4 amyloid precursor gene coding for a possibly
RT secreted protein.";
RL Science 245:651-653(1989).
RN [15]
RP PARTIAL SEQUENCE FROM N.A. (ISOFORM APP695).
RC TISSUE=Brain;
RX MEDLINE=87231971; PubMed=3035574;
RA Robakis N.K., Ramakrishna N., Wolfe G., Wisniewski H.M.;
RT "Molecular cloning and characterization of a cDNA encoding the
RT cerebrovascular and the neuritic plaque amyloid peptides.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:4190-4194(1987).
RN [16]
RP SEQUENCE OF 286-366 FROM N.A.
RX MEDLINE=88122640; PubMed=2893290;
RA Tanzi R.E., McClatchey A.I., Lamperti E.D., Villa-Komaroff L.,
RA Gusella J.F., Neve R.L.;
RT "Protease inhibitor domain encoded by an amyloid protein precursor
RT mRNA associated with Alzheimer's disease.";
RL Nature 331:528-530(1988).
RN [17]
RP SEQUENCE OF 287-367 FROM N.A.
RX MEDLINE=88122641; PubMed=2893291;
RA Kitaguchi N., Takahashi Y., Tokushima Y., Shiojiri S., Ito H.;
RT "Novel precursor of Alzheimer's disease amyloid protein shows
RT protease inhibitory activity.";
RL Nature 331:530-532(1988).
RN [18]
RP SEQUENCE OF 507-770 FROM N.A.
RC TISSUE=Brain cortex;
RX MEDLINE=88124954; PubMed=2593379;
RA Zain S.B., Salim M., Chou W.G., Sajdel-Sulkowska E.M., Majocha R.E.,
RA Marotta C.A.;
RT "Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer
RT disease brain: coding and noncoding regions of the fetal precursor
RT mRNA are expressed in the cortex.";
RL Proc. Natl. Acad. Sci. U.S.A. 85:929-933(1988).
RN [19]
RP SEQUENCE OF 523-555, AND COLLAGEN-BINDING DOMAIN.
RX MEDLINE=96139497; PubMed=8576160;
RA Behr D., Hesse L., Masters C.L., Multhaup G.;
RT "Regulation of amyloid protein precursor (APP) binding to collagen and
RT mapping of the binding sites on APP and collagen type I.";
RL J. Biol. Chem. 271:1613-1620(1996).
RN [20]
RP SEQUENCE OF 655-737 FROM N.A., AND VARIANTS AD PHE-717, AD ILE-717
RP AND AD GLY-717.
RX MEDLINE=93236601; PubMed=8476439;
RA Derman R.B., Rosenczwaig R., Miller D.L.;
RT "A system for studying the effect(s) of familial Alzheimer disease
RT mutations on the processing of the beta-amyloid peptide precursor.";
RL Biochem. Biophys. Res. Commun. 192:196-103(1993).
RN [21]
RP SEQUENCE OF 656-737 FROM N.A.
RX MEDLINE=89392030; PubMed=2675837;
RA Johnstone E.M., Chaney M.O., Moore R.E., Ward K.E., Norris F.H.,
RA Little S.P.;
RT "Alzheimer's disease amyloid peptide is encoded by two exons and shows
RT similarity to soybean trypsin inhibitor.";
RL Biochem. Biophys. Res. Commun. 163:1248-1255(1989).
RN [22]

Query Match 100.0%; Score 57; DB 1; Length 770;
Best Local Similarity 100.0%; Pred. No. 0.0027;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KQYTSIHG 10
|||||
Db 725 KQYTSIHG 734

RESULT 5
A4 MACFA STANDARD; PRT; 770 AA.
AC P53601; Q95N7; 770 AA.
DT 01-CC1-1996 (Rel. 34, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
DE amyloid protein homolog) [Contains: Soluble APP-alpha (S-APP-alpha);
DE Soluble APP-beta (S-APP-beta); C99; Beta-amyloid protein 42 (Beta-
DE APP42); Beta-amyloid protein 40 (Beta-APP40); C83; P3(42); P3(40);
DE Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-CTF(57)
DE (Gamma-secretase C-terminal fragment 57); Gamma-CTF(50) (Gamma-
DE secretase C-terminal fragment 50); C31].
GN APP.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS APP695 AND APP770).
RC TISSUE=Cerebellum;
RX MEDLINE=91273117; PubMed=1905108;
RA Pedlisny M.B., Tolan D.R., Selkoe D.J.;
RT "Homology of the amyloid beta protein precursor in monkey and human
RT supports a primate model for beta amyloidosis in Alzheimer's
RT disease.";
RL Am. J. Pathol. 138:1423-1435(1991).
CC -1- FUNCTION: Functions as a cell surface receptor and performs
CC physiological functions on the surface of neurons relevant to
CC neurite growth, neuronal adhesion and axonogenesis. Involved in
CC cell motility and transcription regulation through protein-protein
CC interactions (By similarity). Can promote transcription activation
CC through binding to APBB1/Tip60 and inhibit Notch signaling through
CC interaction with Numb (By similarity). Couples to apoptosis-
CC inducing pathways such as those mediated by G10 and JIP (By
CC similarity). Inhibits G10 alpha Affase activity (By similarity).
CC Acts as a kinesin I membrane receptor, mediating the axonal
CC transport of beta-secretase and presenilin 1 (By similarity). May
CC be involved in copper homeostasis/oxidative stress through copper
CC ion reduction. In vitro, copper-metalated APP induces neuronal
CC death directly or is potentiated through Cu(II)-mediated low-
CC density lipoprotein oxidation (By similarity). Can regulate
CC neurite outgrowth through binding to components of the
CC extracellular matrix such as heparin and collagen I and IV (By
CC similarity). The splice isoforms that contain the BPTI domain

CC possesses protease inhibitor activity (By similarity).
CC -1- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
CC with metal-reducing activity. Bind transient metals such as
CC copper, zinc and iron (By similarity).
CC -1- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
CC peptides, including C31, are potent enhancers of neuronal
CC apoptosis (By similarity).
CC -1- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
CC cytoplasmic proteins, including APBB family members, the APOA
CC family, MAPK1P1, and SHC1, Numb and Dab1 (By similarity). Binding
CC to Dab1 inhibits its serine phosphorylation (By similarity). Also
CC interacts with GPCR-like protein BFP, FFR11, APPBP1, IBI, KNS2
CC (via its TPR domains) (By similarity), APPB2 (via Bass) and DBL1.
CC In vitro, it binds MAPT via the MT-binding domains (By
CC similarity). Associates with microtubules in the presence of ATP
CC and in a kinesin-dependent manner (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
CC protein that rapidly becomes internalized via clathrin-coated
CC pits. During maturation, the immature APP (N-glycosylated in the
CC endoplasmic reticulum) moves to the Golgi complex where complete
CC maturation occurs (O-glycosylated and sulfated). After alpha-
CC secretase cleavage, soluble APP is released into the extracellular
CC space and the C-terminal is internalized to endosomes and
CC lysosomes. Some APP accumulates in secretory transport vesicles
CC leaving the late Golgi compartment and returns to the cell
CC surface. Gamma-CTF(59) peptide is located to both the cytoplasm
CC and nuclei of neurons (By similarity).
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Comment=Additional isoforms seem to exist;
CC Name=APP770;
CC IsoId=P53601-1; Sequence=Displayed;
CC Name=APP695;
CC IsoId=P53601-2; Sequence=VSP_000010, VSP_000011;
CC -1- DOMAIN: The basolateral sorting signal (BaSS) is required for
CC sorting of membrane proteins to the basolateral surface of
CC epithelial cells (By similarity).
CC -1- DOMAIN: The NPXY sequence motif found in many tyrosine-
CC phosphorylated proteins is required for the specific binding of
CC the PID domain. However additional amino acids either N- or C-
CC terminal to the NPXY motif are often required for complete
CC interaction. The PID domain-containing proteins which bind APP
CC require the YENPTY motif for full interaction. These interactions
CC are independent of phosphorylation on the terminal tyrosine
CC residue. The NPXY site is also involved in clathrin-mediated
CC endocytosis (By similarity).
CC -1- PTM: Proteolytically processed under normal cellular conditions.
CC Cleavage by alpha-secretase or alternatively by beta-secretase
CC leads to generation and extracellular release of soluble APP
CC peptides, S-APP-alpha and S-APP-beta, respectively, and the
CC retention of corresponding membrane-anchored C-terminal fragments,
CC C83 and C99. Subsequent processing of C83 by gamma-secretase
CC yields P3 peptides. This is the major secretory pathway and is
CC nonamyloidogenic. Alternatively, presenilin/nicastrin-mediated
CC gamma-secretase processing of C99 releases the amyloid beta
CC proteins, amyloid-beta 40 (Abeta40) and amyloid-beta 42 (Abeta42),
CC major components of amyloid plaques, and the cytotoxic C-terminal

fragments, gamma-CTF(50), gamma-CTF(57) and gamma-CTF(59) (By similarity).

-|- PM: Proteolytically cleaved by caspases during neuronal apoptosis (By similarity). Cleavage at Asp-739 by either caspase-3, -8 or -9 results in the production of the neurotoxic C31 peptide and the increased production of beta-amyloid peptides (By similarity).

-|- PM: N- and O-glycosylated (By similarity).

-|- PM: Phosphorylation in the C-terminal on tyrosine, threonine and serine residues is neuron-specific. Phosphorylation can affect APP processing, neuronal differentiation and interaction with other proteins (By similarity).

-|- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and zinc, can induce histidine-bridging between beta-amyloid molecules resulting in beta-amyloid-metal aggregates (By similarity). Extracellular zinc-binding increases binding of heparin to APP and inhibits collagen-binding (By similarity).

-|- SIMILARITY: Belongs to the APP family.

-|- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.

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EMBL; M58727; AAA36829.1; -.
 EMBL; M58726; AAA36828.1; -.
 HSSP; P05067; 1AAP.
 InterPro; IPR008135; A4_APP.
 InterPro; IPR008154; A4_extra.
 InterPro; IPR001253; Beta_APP.
 InterPro; IPR002223; Kunitz_BPTI.
 Pfam; PF02177; A4_EXTRA; 1.
 Pfam; PF03494; Beta_APP; 1.
 Pfam; PF00014; Kunitz_BPTI; 1.
 PRINTS; PR00203; AMYLOIDA4.
 PRINTS; PR00739; BASICPTASE.
 ProDom; PD000222; Kunitz_BPTI; 1.
 SMART; SM00006; A4_EXTRA; 1.
 SMART; SM00131; KU; 1.
 PROSITE; PS00319; A4_EXTRA; 1.
 PROSITE; PS00320; A4_INTRA; 1.
 PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 PROSITE; PS00279; BPTI_KUNITZ_2; 1.
 K0 Apoptosis; Endocytosis; Cell adhesion; Serine protease inhibitor; Coated pits; Neurone; Heparin-binding; Metal-binding; Copper; Iron; Zinc; Signal; Transmembrane; Glycoprotein; Phosphorylation; Proteoglycan; Alternative splicing; Amyloid.
 SIGNAL 1 17 BY SIMILARITY.
 FT CHAIN 18 770 AMYLOID BETA A4 PROTEIN.
 FT CHAIN 18 687 SOLUBLE APP-ALPHA (POTENTIAL).
 FT CHAIN 18 671 SOLUBLE APP-BETA (POTENTIAL).
 FT CHAIN 672 770 C99 (POTENTIAL).
 FT CHAIN 672 713 BETA-AMYLOID PROTEIN 42 (POTENTIAL).
 FT CHAIN 672 711 BETA-AMYLOID PROTEIN 40 (POTENTIAL).

FT CHAIN 688 770 C83 (POTENTIAL).
 FT CHAIN 688 713 P3(40) (POTENTIAL).
 FT CHAIN 688 711 GAMMA-CTF(59) (POTENTIAL).
 FT CHAIN 712 770 GAMMA-CTF(57) (POTENTIAL).
 FT CHAIN 714 770 GAMMA-CTF(50) (POTENTIAL).
 FT CHAIN 721 770 C31 (POTENTIAL).
 FT CHAIN 740 770 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 18 699 POTENTIAL.
 FT TRANSMEM 700 723 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 724 770 HEPARIN-BINDING (BY SIMILARITY).
 FT DOMAIN 96 110 ZINC-BINDING (BY SIMILARITY).
 FT DOMAIN 181 188 BPTI/KUNITZ INHIBITOR.
 FT DOMAIN 291 341 HEPARIN-BINDING (BY SIMILARITY).
 FT DOMAIN 391 423 HEPARIN-BINDING (BY SIMILARITY).
 FT DOMAIN 491 522 HEPARIN-BINDING (BY SIMILARITY).
 FT DOMAIN 523 540 COLLAGEN-BINDING (BY SIMILARITY).
 FT DOMAIN 732 751 INTERACTION WITH G(O)-ALPHA (BY SIMILARITY).
 FT DOMAIN 230 260 ASP/GLU-RICH (ACIDIC).
 FT DOMAIN 274 280 POLY-THR.
 FT SITE 144 144 REQUIRED FOR COPPER(II) REDUCTION (BY SIMILARITY).
 FT ACT SITE 301 302 REACTIVE BOND (BY SIMILARITY).
 FT SITE 671 672 CLEAVAGE (BY BETA-SECRETASE) (BY SIMILARITY).
 FT SITE 672 673 CLEAVAGE (BY CASPASE-6) (BY SIMILARITY).
 FT SITE 687 688 CLEAVAGE (BY ALPHA-SECRETASE) (BY SIMILARITY).
 FT SITE 704 704 IMPLICATED IN FREE RADICAL PROPAGATION (BY SIMILARITY).
 FT SITE 706 706 INVOLVED IN OXIDATIVE REACTIONS (BY SIMILARITY).
 FT SITE 711 712 CLEAVAGE (BY GAMMA-SECRETASE; SITE 1) (BY SIMILARITY).
 FT SITE 713 714 CLEAVAGE (BY GAMMA-SECRETASE; SITE 2) (BY SIMILARITY).
 FT SITE 720 721 CLEAVAGE (BY GAMMA-SECRETASE; SITE 3) (BY SIMILARITY).
 FT SITE 724 734 BASOLATERAL SORTING SIGNAL (BY SIMILARITY).
 FT SITE 739 740 CLEAVAGE (BY CASPASES-3,-6,-8 OR -9)

Query Match 100.0%; Score 57; DB 1; Length 770;
 Best Local Similarity 100.0%; Pred. No. 0.0027;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKQYTSIHG 10
 |||||
 Db 725 KKQYTSIHG 734

RESULT 6
 A4_MOUSE STANDARD; PRT; 770 AA.
 ID A4_MOUSE
 AC P12023; P97487; P97942; Q99K32;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)

RP INTERACTION WITH KNS2.
RA MEDLINE=21010507; PubMed=11144355;
RX Kamal A., Sokin G.B., Yang Z., Xia C.-H., Goldstein L.S.;
RT "Axonal transport of amyloid precursor protein is mediated by direct
RT binding to the kinesin light chain subunit of kinesin-1.";
RL Neuron 28:449-459(2000).
[12]
RP C-TERMINAL PROTEIN-PROTEIN INTERACTIONS, AND MUTAGENESIS OF TYR-728;
RX MEDLINE=743; TYR-757; ASN-759 AND TYR-762.
RP MEDLINE=21408156; PubMed=11517249;
RA Matsuda S., Yasukawa T., Honma Y., Ito Y., Niikura T., Hiraki T.,
RA Hirai S., Ono S., Kita Y., Kawasumi M., Kouyama K., Yanamoto T.,
RA Kyriakis J.M., Nishimoto I.,
RT "C-Jun N-terminal kinase (JNK)-interacting protein-1b/islet-brain-1
RT scaffolds Alzheimer's amyloid precursor protein with JNK.";
RL J. Neurosci. 21:6597-6607(2001).
[13]
RP INTERACTION WITH MAPK8IP1, AND PHOSPHORYLATION.
RX MEDLINE=22028091; PubMed=11912189;
RA Taru H., Iijima K.-I., Hase M., Kirino Y., Yagi Y., Suzuki T.;
RT "Interaction of Alzheimer's beta-amyloid precursor family proteins
RT with scaffold proteins of the JNK signaling cascade.";
RL J. Biol. Chem. 277:20070-20078(2002).
[14]
RP INTERACTION OF CTF PEPTIDES WITH NUNB.
RX MEDLINE=22008109; PubMed=12011466;
RA Roncarati R., Sestan N., Scheinfeld M.H., Berechid B.E., Lopez P.A.,
RA Roncarati O., McGlade J.C., Rakic P., D'Adamo L.;
RT "The gamma-secretase-generated intracellular domain of beta-amyloid
RT precursor protein binds Numb and inhibits Notch signaling.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:7102-7107(2002).
[15]
RP GAMMA-SECRETASE PROCESSING, AND INTERACTION WITH APBB1.
RX MEDLINE=21437805; PubMed=11553691;
RA Cupers P., Orlans I., Craessaerts K., Annaert W., De Strooper B.;
RT "The amyloid precursor protein (APP)-cytoplasmic fragment generated by
RT gamma-secretase is rapidly degraded but distributes partially in a
RT nuclear fraction of neurons in culture.";
RL J. Neurochem. 78:1168-1178(2001).
-!- FUNCTION: Functions as a cell surface receptor and performs
physiological functions on the surface of neurons relevant to
neurite growth, neuronal adhesion and axonogenesis. Involved in
cell motility and transcription regulation through protein-protein
interactions. Can promote transcription activation through binding
to APBB1/Tip60 and inhibit Notch signaling through interaction
with Numb. Couples to apoptosis-inducing pathways such as those
mediated by G(O) and JIP. Inhibits G(O) alpha ATPase activity (By
similarity). Acts as a kinesin I membrane receptor, mediating the
axonal transport of beta-secretase and presenilin 1. May be
involved in copper homeostasis/oxidative stress through copper ion
reduction. Can regulate neurite outgrowth through binding to
components of the extracellular matrix such as heparin and
collagen I and IV (By similarity). The splice isoforms that
contain the Bpr1 domain possess protease inhibitor activity (By
similarity).
-!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
with metal-reducing activity. Bind transient metals such as

CC copper, zinc and iron. Rat and mouse beta-amyloid peptides bind
CC only weakly transient metals and have little reducing activity due
CC to substitutions of transient metal chelating residues. Beta-APP42
CC may activate mononuclear phagocytes in the brain and elicit
CC inflammatory responses. Promotes both tau aggregation and TPX 11-
CC mediated phosphorylation (By similarity).
CC -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
CC peptides, including C31, are potent enhancers of neuronal
CC apoptosis.
CC -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
CC cytoplasmic proteins, including APBB family members, the APEA
CC family, MAPK8IP1, SKC1, Numb and Dab1. Binding to Dab1 inhibits
CC its serine phosphorylation. Also interacts with GPCR-like protein
CC BPP, FPR1, APBB1, IBL, KNS2 (via its TPR domains), APBB2 (via
CC Bass) and DBP1 (By similarity). In vitro, it binds MAPT via the
CC MT-binding domains (By similarity). Associates with microtubules
CC in the presence of ATP and in a kinesin-dependent manner (By
CC similarity). Interacts, through a C-terminal domain, with GNAO1
CC (By similarity). Amyloid beta-42 binds CHRNA7 in hippocampal
CC neurons (By similarity). Beta-amyloid associates with HADH2 (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
CC protein that rapidly becomes internalized via clathrin-coated
CC pits. During maturation, the immature APP (N-glycosylated in the
CC endoplasmic reticulum) moves to the Golgi complex where complete
CC Query Match 100.0%; Score 57; DB 1; Length 770;
CC Best Local Similarity 100.0%; Pred.No. 0.0027;
CC Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC QY 1 KQVTSIHG 10
CC DQ 725 KQVTSIHG 734
CC ID A4_PIG STANDARD; PRT; 770 AA.
CC AC P79307; Q29023; Q9TU10;
CC DT 01-NOV-1987 (Rel. 35, Created)
CC DT 10-OCT-2003 (Rel. 42, Last sequence update)
CC DT 10-OCT-2003 (Rel. 42, Last annotation update)
CC DE Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
CC amyloid protein homolog) [Contains: Soluble APP-alpha (S-APP-alpha);
CC Soluble APP-beta (S-APP-beta); C99; Beta-amyloid protein 42 (Beta-
CC APP42); Beta-amyloid protein 40 (Beta-APP40); C83; P3(40);
CC Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-CTF(57)
CC (Gamma-secretase C-terminal fragment 57); Gamma-CTF(50) (Gamma-
CC secretase C-terminal fragment 50); C31].
CC OS Sus scrofa (Pig).
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
CC OX NCBI_TaxID=9923;
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RA Kimura A., Takanashi T.;
CC RT "Amyloid precursor protein 770.";

Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.

[2]
 CC SEQUENCE OF 1-136 FROM N.A.
 CC TISSUE=Small intestine;
 CC RA Witterhoe A.K., Fredholm M.;
 CC RT "Evaluation and characterization of a porcine small intestine cDNA
 CC RT library.";
 CC RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 CC [3]
 CC SEQUENCE OF 667-723 FROM N.A.
 CC TISSUE=Brain;
 CC RA MEDLINE=92017079; PubMed=1656157;
 CC RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
 CC RT "Conservation of the sequence of the Alzheimer's disease amyloid
 CC RT peptide in dog, polar bear and five other mammals by cross-species
 CC RT polymerase chain reaction analysis.";
 CC RL Brain Res. Mol. Brain Res. 10:299-305 (1991).
 CC
 CC -|- FUNCTION: Functions as a cell surface receptor and performs
 CC physiological functions on the surface of neurons relevant to
 CC neurite growth, neuronal adhesion and axonogenesis. Involved in
 CC cell motility and transcription regulation through protein-protein
 CC interactions (By similarity). Can promote transcription activation
 CC through binding to APBB1/tip60 and inhibit Notch signaling through
 CC interaction with Numb (By similarity). Couples to apoptosis-
 CC inducing pathways such as those mediated by G(O) and JIP (By
 CC similarity). Inhibits G(O) alpha ATPase activity (By similarity).
 CC Acts as a kinesin I membrane receptor, mediating the axonal
 CC transport of beta-secretase and presenilin 1 (By similarity). May
 CC be involved in copper homeostasis/oxidative stress through copper
 CC ion reduction (By similarity). In vitro, copper-metallated APP
 CC induces neuronal death directly or is potentiated through Cu(II)-
 CC mediated low-density lipoprotein oxidation (By similarity). Can
 CC regulate neurite outgrowth through binding to components of the
 CC extracellular matrix such as heparin and collagen I and IV (By
 CC similarity).
 CC
 CC -|- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
 CC with metal-reducing activity. Bind transient metals such as
 CC copper, zinc and iron (By similarity).
 CC
 CC -|- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
 CC peptides, including C31, are potent enhancers of neuronal
 CC apoptosis (By similarity).
 CC
 CC -|- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
 CC cytoplasmic proteins, including APBB family members, the APBA
 CC family, MAPKIP1, and SHC1, Numb and Dab1 (By similarity). Binding
 CC to Dab1 inhibits its serine phosphorylation (By similarity). Also
 CC interacts with GPCR-like protein EPP, FPR1, APBB1, IBI, KNS2
 CC (via its TPR domains) (By similarity), APPB2 (via BASS) and DBP1.
 CC In vitro, it binds MAPT via the MT-binding domains (By
 CC similarity). Associates with microtubules in the presence of ATP
 CC and in a kinesin-dependent manner (By similarity).
 CC
 CC -|- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
 CC protein that rapidly becomes internalized via clathrin-coated
 CC pits. During maturation, the immature APP (N-glycosylated in the
 CC endoplasmic reticulum) moves to the Golgi complex where complete
 CC maturation occurs (O-glycosylated and sulfated). After alpha-
 CC secretase cleavage, soluble APP is released into the extracellular
 CC space and the C-terminal is internalized to endosomes and

lysosomes. Some APP accumulates in secretory transport vesicles
 leaving the late Golgi compartment and returns to the cell
 surface. Gamma-CTF(59) peptide is located to both the cytoplasm
 and nuclei of neurons (By similarity).
 -|- DOMAIN: The basolateral sorting signal (BASS) is required for
 sorting of membrane proteins to the basolateral surface of
 epithelial cells (By similarity).
 -|- DOMAIN: The NPXY sequence motif found in many tyrosine-
 phosphorylated proteins is required for the specific binding of
 the PID domain. However additional amino acids either N- or C-
 terminal to the NPXY motif are often required for complete
 interaction. The PID domain-containing proteins which bind APP
 require the YENPTY motif for full interaction. These binding
 are independent of phosphorylation on the terminal tyrosine
 residue. The NPXY site is also involved in clathrin-mediated
 endocytosis (By similarity).
 -|- PTM: Proteolytically processed under normal cellular conditions.
 Cleavage by alpha-secretase or alternatively by beta-secretase
 leads to generation and extracellular release of soluble APP
 peptides, s-APP-alpha and s-APP-beta, respectively, and the
 retention of corresponding membrane-anchored C-terminal fragments,
 C83 and C99. Subsequent processing of C83 by gamma-secretase
 yields p3 peptides. This is the major secretory pathway and is
 nonamyloidogenic. Alternatively, presenilin/nicastrin-mediated
 gamma-secretase processing of C99 releases the amyloid beta
 proteins, amyloid-beta 40 (Abeta40) and amyloid-beta 42 (Abeta42),
 major components of amyloid plaques, and the cytotoxic C-terminal
 fragments, gamma-CTF(50), gamma-CTF(57) and gamma-CTF(59) (By
 similarity).
 -|- PTM: Proteolytically cleaved by caspases during neuronal apoptosis
 (By similarity). Cleavage at Asp-739 by either caspase-3, -8 or -9
 results in the production of the neurotoxic C31 peptide and the
 increased production of beta-amyloid peptides (By similarity).
 -|- PTM: N- and O-glycosylated (By similarity).
 -|- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and
 serine residues is neuron-specific. Phosphorylation can affect APP
 processing, neuronal differentiation and interaction with other
 proteins (By similarity).
 -|- PTM: Extracellular binding and reduction of copper, results in a
 corresponding oxidation of Cys-144 and Cys-158, and the formation
 of a disulfide bond (By similarity).
 -|- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and
 zinc, can induce histidine-bridging between beta-amyloid molecules
 resulting in beta-amyloid-metal aggregates (By similarity).
 Extracellular zinc-binding increases binding of heparin to APP and
 inhibits collagen-binding (By similarity).
 -|- SIMILARITY: Belongs to the APP family.
 -|- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.

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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC -----

DR EMBL; AB032550; BAB4580.1; -.
DR EMBL; Z84022; CAB06313.1; -.
DR EMBL; X56127; CAA39592.1; -.
DR HSSP; P05067; IAAP.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR008154; A4_extra.
DR InterPro; IPR002223; Kunitz_BPTI.
DR Pfam; PF02177; A4_EXTRA; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Kunitz_BPTI; 1.
DR SMART; SM00006; A4_EXTRA; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
KW Apoptosis; Endocytosis; Cell adhesion; Serine protease inhibitor;
KW Coated pits; Neurone; Heparin-binding; Metal-binding; Copper; Iron;
KW Zinc; Signal; Transmembrane; Glycoprotein; Phosphorylation;
KW Amyloid.
FT SIGNAL 1 17 BY SIMILARITY.
FT CHAIN 18 770 AMYLOID BETA A4 PROTEIN.
FT CHAIN 18 687 SOLUBLE APP-ALPHA (POTENTIAL).
FT CHAIN 18 671 SOLUBLE APP-BETA (POTENTIAL).
FT CHAIN 672 770 C99 (BY SIMILARITY).
FT CHAIN 672 713 BETA-AMYLOID PROTEIN 42 (BY SIMILARITY).
FT CHAIN 672 711 BETA-AMYLOID PROTEIN 40 (BY SIMILARITY).
FT CHAIN 688 770 C83 (BY SIMILARITY).
FT CHAIN 688 713 P3(42) (BY SIMILARITY).
FT CHAIN 688 711 P3(40) (BY SIMILARITY).
FT CHAIN 712 770 GAMMA-CTF(59).
FT CHAIN 714 770 GAMMA-CTF(57).
FT CHAIN 721 770 GAMMA-CTF(50) (BY SIMILARITY).
FT CHAIN 740 770 C31 (DURING APOPTOSIS) (BY SIMILARITY).
FT DOMAIN 18 699 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 700 723 POTENTIAL.
FT DOMAIN 724 770 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 96 110 HEPARIN-BINDING (BY SIMILARITY).
FT DOMAIN 135 153 COPPER-BINDING (BY SIMILARITY).
FT DOMAIN 161 188 ZINC-BINDING (BY SIMILARITY).
FT DOMAIN 291 341 BPTI/KUNITZ INHIBITOR.
FT DOMAIN 391 423 HEPARIN-BINDING (BY SIMILARITY).
FT DOMAIN 451 522 HEPARIN-BINDING (BY SIMILARITY).
FT DOMAIN 523 540 COLLAGEN-BINDING (BY SIMILARITY).
FT DOMAIN 732 751 INTERACTION WITH G(O)-ALPHA (BY SIMILARITY).
FT DOMAIN 230 260 ASP/GLU-RICH (ACIDIC).
FT DOMAIN 274 280 POLY-THR.
FT SITE 144 144 REQUIRED FOR COPPER(II) REDUCTION (BY SIMILARITY).
FT ACT SITE 301 302 REACTIVE BOND (BY SIMILARITY).
FT SITE 671 672 CLEAVAGE (BY BETA-SECRETASE) (BY SIMILARITY).
FT SITE 672 673 CLEAVAGE (BY CASPASE-6) (BY SIMILARITY).
FT SITE 687 688 CLEAVAGE (BY ALPHA-SECRETASE) (BY SIMILARITY).
FT

FT SITE 704 704 IMPLICATED IN FREE RADICAL PROPAGATION (BY SIMILARITY).
FT SITE 706 706 INVOLVED IN OXIDATIVE REACTIONS (BY SIMILARITY).
FT SITE 711 712 CLEAVAGE (BY GAMMA-SECRETASE; SITE 1) (BY SIMILARITY).
FT SITE 713 714 CLEAVAGE (BY GAMMA-SECRETASE; SITE 2) (BY SIMILARITY).
FT SITE 720 721 CLEAVAGE (BY GAMMA-SECRETASE; SITE 3)

Query Match 100.0% Score 57; DB 1; Length 770;
Best Local Similarity 100.0% Pred. No. 0.0027;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKQYTSIHG 10
|||||||
Db 725 KKQYTSIHG 734

RESULT 8
A4_RAT ID A4_RAT STANDARD; PRT; 770 AA.
AC P06592;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Amyloid beta A4 protein precursor (APP) (Alzheimer's disease amyloid protein homolog) (Amyloidogenic glycoprotein) (AG) [Contains: Soluble APP-alpha (S-APP-alpha); Soluble APP-beta (S-APP-beta); C99; Beta-amyloid protein 42 (Beta-APP42); Beta-amyloid protein 40 (Beta-APP40); C83; P3(42); P3(40); Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-CTF(57) (Gamma-secretase C-terminal fragment 57); Gamma-CTF(50) (Gamma-secretase C-terminal fragment 50); C31].
GN APP.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM APP695).
RC TISSUE=Brain;
RX MEDLINE=88312583; PubMed=2900758;
RA Shivers B.D., Hilbich C., Multhaup G., Salbaum J.M., Beyreuther K., Seeburg P.H.;
RT "Alzheimer's disease amyloidogenic glycoprotein: expression pattern in rat brain suggests a role in cell contact";
RL EMBO J. 7:11365-1370(1988).
RN [2]
RP SEQUENCE OF 289-364 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=89183625; PubMed=2648331;
RA Kang J., Mueller-Hill B.;
RT "The sequence of the two extra exons in rat preA4";
RL Nucleic Acids Res. 17:2130-2130(1989).
RN [3]
RP SEQUENCE OF 720-730, AND MASS SPECTROMETRY.
RX MEDLINE=21443797; PubMed=11463586;

RA Cu Y., Misonou H., Sato T., Domae N., Takio K., Ihara Y.;
 RT "Distinct intramembrane cleavage of the beta-amyloid precursor protein
 RT family resembling gamma-secretase-like cleavage of Notch.";
 RL J. Biol. Chem. 276:35235-35238(2001).
 RN [4]
 RP ALTERNATIVE SPLICING.
 RX MEDLINE=96187032; PubMed=8624099;
 RA Sandbrink R., Masters C.L., Beyreuther K.;
 RT "APP gene family. Alternative splicing generates functionally related
 RT isoforms.";
 RL Ann. N.Y. Acad. Sci. 777:281-287(1996).
 RN [5]
 RP TISSUE SPECIFICITY OF APPICAN.
 RX MEDLINE=95263526; PubMed=7744833;
 RA Shioi J., Pangalos M.N., Ripellino J.A., Vassilacopoulos D.,
 RA Mytilinou C., Margolis R.U., Robakis N.K.;
 RT "The Alzheimer amyloid precursor proteoglycan (appican) is present in
 RT brain and is produced by astrocytes but not by neurons in primary
 RT neural cultures.";
 RL J. Biol. Chem. 270:11839-11844(1995).
 RN [6]
 RP TISSUE SPECIFICITY OF ISOFORMS.
 RX MEDLINE=97150061; PubMed=8996834;
 RA Sandbrink R., Monning U., Masters C.L., Beyreuther K.;
 RT "Expression of the APP gene family in brain cells, brain development
 RT and aging.";
 RL Gerontology 43:119-131(1997).
 RN [7]
 RP INTERACTION WITH DBP1, AND MUTAGENESIS OF TYR-757; ASN-759 AND
 TYR-762.
 RX MEDLINE=99127916; PubMed=9930726;
 RA Watanabe T., Sukegawa J., Iomita S., Iijima K.-I., Oguchi S.,
 RA Suzuki T., Nairn A.C., Greengard P.;
 RT "A 127-kDa protein (UV-DBP) binds to the cytoplasmic domain of the
 RT Alzheimer's amyloid precursor protein.";
 RL J. Neurochem. 72:549-556(1999).
 RN [8]
 RP INTERACTION WITH GNAO1, AND MUTAGENESIS OF 732-HIS-733.
 RX MEDLINE=99162676; PubMed=10024358;
 RA Brouillet E., Tremblieu A., Galanaud D., Volovitch M., Bouillot C.,
 RA Valenza C., Prochiantz A., Allinquant B.;
 RT "The amyloid precursor protein interacts with Gq heterotrimeric
 RT protein within a cell compartment specialized in signal
 RT transduction.";
 RL J. Neurosci. 19:1717-1727(1999).
 RN [9]
 RP CHARACTERISTICS OF APPICAN, AND MUTAGENESIS OF SER-656.
 RX MEDLINE=95256193; PubMed=7737970;
 RA Pangalos M.N., Efthymiopoulos S., Shioi J., Robakis N.K.;
 RT "The chondroitin sulfate attachment site of appican is formed by
 RT splicing out exon 15 of the amyloid precursor gene.";
 RL J. Biol. Chem. 270:10368-10391(1995).
 RN [10]
 RP BETA-AMYLOID METAL-BINDING.
 RX MEDLINE=99316162; PubMed=10386999;
 RA Huang X., Atwood C.S., Hartshorn M.A., Multhaup G., Goldstein L.E.,
 RA Scarpa R.C., Cuajungco M.P., Gray D.N., Lim J., Moir R.D., Tanzi R.E.,

RA Bush A.I.;
 RT "The A beta peptide of Alzheimer's disease directly produces hydrogen
 RT peroxide through metal ion reduction.";
 RL Biochemistry 38:7609-7616(1999).
 RN [11]
 RP BETA-AMYLOID ZINC BINDING.
 RX MEDLINE=99343552; PubMed=10413512;
 RA Liu S.T., Howlett G., Barrow C.J.;
 RT "Histidine-13 is a crucial residue in the zinc ion-induced aggregation
 RT of the A beta peptide of Alzheimer's disease.";
 RL Biochemistry 38:9373-9378(1999).
 RN [12]
 RP IMPORTANCE OF GLY-704 IN FREE RADICAL PROPAGATION, AND MUTAGENESIS OF
 GLY-704.
 RX MEDLINE=21956095; PubMed=11959460;
 RA Kanski J., Varadarajan S., Aksenova M., Butterfield D.A.;
 RT "Role of glycine-33 and methionine-35 in Alzheimer's amyloid beta-
 RT peptide 1-42-associated oxidative stress and neurotoxicity.";
 RL Biochim. Biophys. Acta 1586:190-198(2001).
 RN [13]
 RP PHOSPHORYLATION.
 RX MEDLINE=97239592; PubMed=9085254;
 RA Oishi M., Nairn A.C., Czernik A.J., Lim G.S., Isohara T., Gandy S.E.,
 RA Greengard P., Suzuki T.;
 RT "The cytoplasmic domain of Alzheimer's amyloid precursor protein is
 RT phosphorylated at Thr654, Ser655, and Thr666 in adult rat brain and
 RT cultured cells.";
 RL Mol. Med. 3:111-123(1997).
 RN [14]
 RP PHOSPHORYLATION ON SER-730.
 RX MEDLINE=99262094; PubMed=10329382;
 RA Isohara T., Horiuchi A., Watanabe T., Ando K., Czernik A.J., Uno I.,
 RA Greengard P., Nairn A.C., Suzuki T.;
 RT "Phosphorylation of the cytoplasmic domain of Alzheimer's beta-amyloid
 RT precursor protein at Ser655 by a novel protein kinase.";
 RL Biochem. Biophys. Res. Commun. 258:300-305(1999).
 RN [15]
 RP PHOSPHORYLATION, INDUCTION, SUBCELLULAR LOCATION, AND MUTAGENESIS OF
 THR-743.
 RX MEDLINE=99274744; PubMed=10341243;
 RA Ando K., Oishi M., Takeda S., Iijima K.-I., Isohara T., Nairn A.C.,
 RA Kirino Y., Greengard P., Suzuki T.;
 RT "Role of phosphorylation of Alzheimer's amyloid precursor protein
 RT during neuronal differentiation.";
 RL J. Neurosci. 19:4421-4427(1999).
 RN [16]
 RP PHOSPHORYLATION ON THR-743.
 RX MEDLINE=20396183; PubMed=10936190;
 RA Iijima K.-I., Ando K., Takeda S., Satch Y., Seki T., Itohara S.,
 RA Greengard P., Kirino Y., Nairn A.C., Suzuki T.;
 RT "Neuron-specific phosphorylation of Alzheimer's beta-amyloid precursor
 RT protein by cyclin-dependent kinase 5.";
 RL J. Neurochem. 75:1085-1091(2000).
 RN [17]
 RP CARBOHYDRATE STRUCTURE OF APPICAN.
 RX MEDLINE=21463085; PubMed=11479316;

RA Tsuchida K., Shioi J., Yamada S., Boghosian G., Wu A., Cai H.,
RA Sugahara K., Robakis N.K.:
RT "Appian, the proteoglycan form of the amyloid precursor protein,
RT contains chondroitin sulfate E in the repeating disaccharide region
RL and 4-O-sulfated galactose in the linkage region.";
RL J. Biol. Chem. 276:37155-37160(2001).
CC -!- FUNCTION: Functions as a cell surface
CC physiological functions on the surface of neurons and performs
CC neurite growth, neuronal adhesion and axonogenesis. Involved in
CC cell motility and transcription regulation through protein-protein
CC interactions (By similarity). Can promote transcription activation
CC through binding to APBB1/Tip60 and inhibit Notch signaling through
CC interaction with Numb (By similarity). Couples to apoptosis-
CC inducing pathways such as those mediated by G10 and JIP. Inhibits
CC G10 alpha Arpase activity. Acts as a kinesin I membrane receptor,
CC mediating the axonal transport of beta-secretase and presenilin 1
CC (By similarity). May be involved in copper homeostasis/oxidative
CC stress through copper ion reduction. Can regulate neurite
CC outgrowth through binding to components of the extracellular
CC matrix such as heparin and collagen I and IV (By similarity). The
CC splice isoforms that contain the BPTI domain possess protease
CC inhibitor activity (By similarity).
CC -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
CC with metal-reducing activity. Bind transient metals such as
CC copper, zinc and iron. Rat and mouse beta-amyloid peptides bind
CC only weakly transient metals and have little reducing activity due
CC to substitutions of transient metal chelating residues. Beta-APP42
CC may activate mononuclear phagocytes in the brain and elicit
CC inflammatory responses. Promotes both tau aggregation and TRK II-
CC mediated phosphorylation (By similarity).
CC -!- FUNCTION: Appicans elicit adhesion of neural cells to the
CC extracellular matrix and may regulate neurite outgrowth in the
CC brain.
CC -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
CC peptides, including C31, are potent enhancers of neuronal
CC apoptosis (By similarity).
CC -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
CC cytoplasmic proteins, including APBB family members, the APBA
CC family, MAPKBP1, SHC1 and Numb and Dab1 (By similarity). Binding
CC to Dab1 inhibits its serine phosphorylation (By similarity). Also
CC interacts with GPCR-like protein BPP, FPR1, APPBP1, IBL, KNS2
CC (via its TPR domains), APPBP2 (via BASS) (By similarity) and DBP1.
CC In vitro, it binds NAFT via the MT-binding domains (By
CC similarity). Associates with microtubules in the presence of ATP
CC and in a kinesin-dependent manner (By similarity). Interacts,
CC through a C-terminal domain, with GNAO1. Amyloid beta-42 binds
CC CHRNA7 in hippocampal neurons (By similarity). Beta-amyloid
CC associates with HADH2 (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
CC protein that rapidly becomes internalized via clathrin-coated
CC pits. During maturation, the immature APP (N-glycosylated in the

Query Match 100.04; Score 57; DB 1; Length 770;
Best Local Similarity 100.04; Pred. No. 0.0027;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KQYTSIHGG 10

Db 725 KQYTSIHGG 734
|||||||
RESULT 9
A4_TETFL
ID A4_TETFL STANDARD; PRT; 780 AA.
AC 073683;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog precursor [Contains:
DE Beta-amyloid protein (Beta-APP) (A-beta)].
GN APP.
OS Tetraodon fluviatilis (Puffer fish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorphae; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=47145;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98252138; PubMed=9599080;
RA Villard L., Tassone F., Crnogorac-Jurcovic T., Clancy K., Gardiner K.;
RT "Analysis of pufferfish homologues of the AT-rich human APP gene";
RL Gene 210:17-24(1998).
CC -!- FUNCTION: Functional neuronal receptor which couples to
CC intracellular signaling pathway through the GTP-binding protein
CC G10 (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Belongs to the APP family.
CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC
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CC
CC EMBL; AF018165; AAC41275.1; -.
CC HSPB; P05067; I423.
CC InterPro; IPR008155; A4_APP.
CC InterPro; IPR008154; A4_extra.
CC InterPro; IPR001255; Beta-APP.
CC InterPro; IPR002223; Kunitz_BPTI.
CC Pfam; PF02177; A4_EXTRA; 1.
CC Pfam; PF03494; Beta-APP; 1.
CC Pfam; PF00014; Kunitz_BPTI; 1.
CC PRINTS; PR00203; AMYLOIDA4.
CC PRINTS; PR00759; BASICPTASE.
CC ProDom; PD000222; Kunitz_BPTI; 1.
CC SMART; SM00006; A4_EXTRA; 1.
CC SMART; SM00331; K07; 1.
CC PROSITE; PS00319; A4_EXTRA; 1.
CC PROSITE; PS00320; A4_INTRA; 1.

DR PROSITE; P800280; BPTI_KUNITZ_1; FALSE_NEG.
 DR PROSITE; P850279; BPTI_KUNITZ_2; 1.
 KW Glycoprotein; Amyloid; Neurone; Transmembrane; Signal;
 FT SIGNAL 1 18 POTENTIAL.
 FT CHAIN 19 780 ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN
 FT CHAIN 692 724 HOMOLOG.
 FT DOMAIN 19 711 BETA-AMYLOID PROTEIN (POTENTIAL).
 FT TRANSFEM 712 732 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 733 780 POTENTIAL.
 FT DOMAIN 323 382 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 769 772 BPTI/KUNITZ INHIBITOR.
 FT SITE 327 378 CLATHRIN-BINDING (BY SIMILARITY).
 FT DISULFID 336 361 BY SIMILARITY.
 FT DISULFID 336 361 BY SIMILARITY.
 FT CARBOHYD 560 560 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 780 AA; 88238 MW; 60071BE94520191D CRC64;

Query Match 100.0%; Score 57; DB 1; Length 780;
 Best Local Similarity 100.0%; Pred. No. 0.0027;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KQYTSIHGG 10
 |||||
 Db 735 KQYTSIHGG 744

RESULT 10
 NUAN_LUMTE STANDARD; PRT; 452 AA.
 AC Q34949;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE NADH-ubiquinone oxidoreductase chain 4 (EC 1.6.5.3).
 GN ND4.
 OS Lumbricus terrestris (Common earthworm).
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Annelida; Clitellata; Oligochaeta; Haplotaxida;
 OC Lumbricina; Lumbricidae; Lumbricus.
 OX NCBI_TaxID=6398;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96042914; PubMed=8536978;
 RA Boore J.L., Brown W.M.;
 RT "Complete sequence of the mitochondrial DNA of the annelid worm
 Lumbricus terrestris";
 RL Genetics 141:305-319(1995).
 CC -/- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
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CC -----
 DR EMBL; U24570; AAC46873.1; -.
 DR PIR; S58994; S58994.
 DR InterPro; IPR003918; NADHub_oxred4.
 DR InterPro; IPR003916; NADHub_oxred5.
 DR InterPro; IPR001750; Oxidored_q1.
 DR InterPro; IPR002600; Oxidored_q5_N.
 DR Pfam; PF00361; oxidored_q1; 1.
 DR Pfam; PF01059; oxidored_q5_N; 1.
 DR PRINTS; PR01434; NADHGNASES.
 DR PRINTS; PR01437; NUOXORDTASE4.
 KW Oxidoreductase; NAD; Ubiquinone; Mitochondrion.
 SQ SEQUENCE 452 AA; 50482 MW; 604CF0F63129DEDE CRC64;

Query Match 66.4%; Score 39; DB 1; Length 452;
 Best Local Similarity 85.7%; Pred. No. 4.8;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 YTSIHGG 10
 |||||
 Db 405 YTSIHGG 411

RESULT 11
 ISPH_SYNY3 STANDARD; PRT; 379 AA.
 AC Q55643; Q55066;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE 4-hydroxy-3-methylbut-2-enyl diphosphate reductase (EC 1.17.1.2).
 GN ISPH OR LYTB OR SLR0348.
 OS Synechocystis sp. (strain PCC 6803).
 OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
 OX NCBI_TaxID=1148;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97449302; PubMed=9305771;
 RA Cassier-Chauvat C., Poncelet M., Chauvat F.;
 RT "Three insertion sequences from the cyanobacterium Synechocystis
 PCC6803 support the occurrence of horizontal DNA transfer among
 bacteria";
 RL Gene 195:257-266(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96127529; PubMed=8590279;
 RA Kaneko T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N.,
 RA Sugita M., Tabata S.;
 RT "Sequence analysis of the genome of the unicellular cyanobacterium
 Synechocystis sp. strain PCC6803. I. Sequence features in the 1 MD
 DNA Res. 2:153-166(1995).
 RN [3]
 RP PATHWAY.
 RX MEDLINE=20461233; PubMed=11004185;
 RA Cunningham F.X. Jr., Laford T.P., Gantt E.;
 RT "Evidence of a role for LytB in the nonmevalonate pathway of

RT isoprenoid biosynthesis.";
 RL J. Bacteriol. 182:5841-5848(2000).
 CC -!- FUNCTION: Converts 1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate
 CC into isopentenyl diphosphate (IPP) and dimethylallyl diphosphate
 CC (DMAPP).
 CC -!- CATALYTIC ACTIVITY: Isopentenyl diphosphate + NAD(P)(+) + H(2)O =
 CC (E)-4-hydroxy-3-methylbut-2-en-1-yl diphosphate + NAD(P)H.
 CC -!- PATHWAY: Nonmevalonate terpenoid biosynthesis pathway; seventh
 CC (last) step.
 CC -!- SIMILARITY: Belongs to the isph family.
 CC
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 CC
 DR EMBL; U38915; AAB72119.1; -;
 DR EMBL; D64000; BAA10159.1; ALT_INIT.
 DR HANAP; MF_00191; -; 1.
 DR InterPro; IPR003451; Lyt-B.
 DR Pfam; PF02401; LytB; 1.
 DR TIGRfam; TIGR00216; isph_lytB; 1.
 KW Isoprene biosynthesis; Complete Proteome; Oxidoreductase; NADP.
 SQ SEQUENCE 379 AA; 42415 MW; 4CD0167AF5D4957E CRC64;
 Query Match 66.7%; Score 38; DB 1; Length 379;
 Best Local Similarity 70.0%; Pred. No. 6.2;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 KQYTSIHG 10
 DB 145 KKEHTSIHG 154
 RESULT 12
 YGM9 YEAST
 ID YGM9 YEAST STANDARD; PRT; 488 AA.
 AC Q01163;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Hypothetical 55.6 kDa protein in CEG1-SOH1 intergenic region.
 GN YGL129C OR G2856.
 OS Saccharomyces cerevisiae (Baker's yeast).
 CC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 CC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96287651; PubMed=8686378;
 RA Rodriguez-Belmonte E., Rodriguez Torres A.M., Tizon B., Cadahia J.L.,
 RA Gonzalez-Siso I., Ramil E., Becerra M., Gonzalez-Dominguez M.,
 RA Cerdan E.;
 RT "Sequence analysis of a 10 kb DNA fragment from yeast chromosome VII

RT reveals a novel member of the DnaJ family.";
 RL Yeast 12:145-148(1996).
 RN [2]
 RP SEQUENCE OF 39-488 FROM N.A.
 RC STRAIN=DSB939;
 RX MEDLINE=92250598; PubMed=1315757;
 RA Shibagaki Y., Itoh N., Yamada H., Nagata S., Mizumoto K.;
 RT "mRNA capping enzyme. Isolation and characterization of the gene
 RT encoding mRNA guanylyltransferase subunit from Saccharomyces
 RT cerevisiae.";
 RL J. Biol. Chem. 267:9521-9528(1992).
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 CC
 DR EMBL; X87252; CAA60702.1; -;
 DR EMBL; Z72651; CAA96938.1; -;
 DR EMBL; D10263; BAA01104.1; -;
 DR PIR; S64140; S64140.
 DR GeneOnline; 141177; -;
 DR SGD; S0003097; RSM23.
 DR GO; GO:0005763; Mitochondrial small ribosomal subunit; IDA.
 DR GO; GO:0003735; Protein constituent of ribosome; IDA.
 DR GO; GO:0006412; Protein biosynthesis; IDA.
 KW Hypothetical protein; ATP-binding.
 FT NP_BIND 188 195 ATP (POTENTIAL).
 SQ SEQUENCE 488 AA; 55562 MW; C59B8AA8658BEA18 CRC64;
 Query Match 66.7%; Score 38; DB 1; Length 488;
 Best Local Similarity 75.0%; Pred. No. 8.1;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 2 KQYTSIHG 9
 DB 137 KQYKSLHH 144
 RESULT 13
 Y4KQ RHISN
 ID Y4KQ RHISN STANDARD; PRT; 142 AA.
 AC P55535;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Very hypothetical 15.3 kDa protein Y4KQ.
 GN Y4KQ.
 OS Rhizobium sp. (strain NGR234).
 OG Plasmid sym pNGR234a.
 CC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 CC Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium.
 OX NCBI_TaxID=394;
 RN [1]

RP SEQUENCE FROM N.A.
RX MEDLINE=97305956; PubMed=9163424;
RA Freiberg C.A., Fellay R., Balroch A., Broughton W.J., Rosenthal A.,
RA Perret X.; basis of symbiosis between Rhizobium and legumes.";
RT "Molecular basis of symbiosis between Rhizobium and legumes.";
RL Nature 387:394-401(1997).
CC -|- SIMILARITY: NONE OBVIOUS. COULD BE A FRAGMENT.
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CC
CC EMBL: AEO00082; AAB91748.1; -.
DR PIR: T10871; T10871.
DR Hypothetical protein; Plasmid.
KW SEQUENCE 142 AA; 15332 MW; 4277C68DD33E8DF1 CRC64;
SQ

Query Match 64.9%; Score 37; DB 1; Length 142;
Best Local Similarity 60.0%; Pred. No. 3.3;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KKYTSIHG 10
|: ||:||||
Db 127 KRSGTSLHG 136

RESULT 14
CYOB BUCAP
ID CYOB BUCAP STANDARD; PRT; 659 AA.
AC Q8K994;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ubiquinol oxidase polypeptide I (EC 1.10.3.-) (Cytochrome O subunit 1)
DE (Oxidase BO(3) subunit 1) (Cytochrome O ubiquinol oxidase subunit 1).
GN CYOB OR BUG5455.
OS Buchnera aphidicola (subsp. Schizaphis graminum).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Buchnera.
OX NCBI_TaxID=98754;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22084549; PubMed=12089438;
RA Tamás I., Klaesson L., Carbaeck B., Naeslund A.K., Eriksson A.-S.,
RA Wernegreen J.J., Sandstrom J.P., Moran N.A., Andersson S.G.E.;
RT "50 million years of genomic stasis in endosymbiotic bacteria.";
RL Science 296:2376-2379(2002).
CC -|- FUNCTION: Cytochrome O terminal oxidase complex is the component
CC of the aerobic respiratory chain that predominates when cells are
CC grown at high aeration. This ubiquinol oxidase shows proton pump
CC activity across the membrane in addition to the electron transfer
CC (By similarity).
CC -|- CATALYTIC ACTIVITY: Ubiquinol-8 + O(2) = Ubiquinone-8 + H(2)O.

CC -|- COFACTOR: Contains two protoheme IX (heme B55 and B562) and
CC copper B (By similarity).
CC -|- PATHWAY: Ubiquinol oxidase catalyzes the terminal step in the
CC electron transport chain.
CC -|- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -|- SIMILARITY: Belongs to the heme-copper respiratory oxidase family.
CC
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CC
CC EMBL: AEO14121; AAM67998.1; -.
DR InterPro: IPR000883; COX1.
DR Pfam: PF00115; COX1; 1.
DR PRINTS: PR01165; CYCOKIDASE1.
DR PROSITE: PS00077; COX1; 1.
KW Oxidoreductase; Respiratory chain; Transmembrane; Heme; Copper;
KW Hydrogen ion transport; Complete proteome.
FT DOMAIN 1 14
FT TRANSMEM 15 35
FT TRANSMEM 36 58
FT TRANSMEM 59 79
FT TRANSMEM 80 106
FT TRANSMEM 107 127
FT TRANSMEM 128 145
FT TRANSMEM 146 166
FT TRANSMEM 167 189
FT TRANSMEM 190 210
FT TRANSMEM 211 225
FT TRANSMEM 226 246
FT TRANSMEM 247 277
FT TRANSMEM 278 298
FT TRANSMEM 299 309
FT TRANSMEM 310 330
FT TRANSMEM 331 347
FT TRANSMEM 348 368
FT TRANSMEM 369 380
FT TRANSMEM 381 401
FT TRANSMEM 402 413
FT TRANSMEM 414 434
FT TRANSMEM 435 456
FT TRANSMEM 457 477
FT TRANSMEM 478 490
FT TRANSMEM 491 511
FT TRANSMEM 512 580
FT TRANSMEM 581 601
FT TRANSMEM 602 605
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FT METAL 334 334 COPPER B (PROBABLE).
FT METAL 419 419 IRON (HEME O AXIAL LIGAND) (PROBABLE).
FT METAL 421 421 IRON (HEME B AXIAL LIGAND) (PROBABLE).
FT CROSSLINK 284 288 1'-histidyl-3'-tyrosine (His-Tyr)
(By similarity).
SQ SEQUENCE 659 AA; 75028 MW; 23D6FB4B04732D23 CRC64;

Query Match 63.2%; Score 36; DB 1; Length 659;
Best Local Similarity 75.0%; Pred. No. 28;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKQYTSIH 8
||||:||||
Db 576 KKQYSAIH 583

RESULT 15

YRDE_CAEEL
ID YRDE_CAEEL STANDARD; PRT; 1268 AA.
AC Q09575;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 26-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical protein K02A2.6 in chromosome II.
GN K02A2.6.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematozoa; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol NZ;
RA Hallsworth K.;
RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: WEAK, TO RETROVIRUS-RELATED POLYPROTEIN.
CC -!- SIMILARITY: Contains 1 CCHC-type zinc finger.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----
CC EMBL; U23171; AAC46707.1; -;
DR PIR; B88209; B88209.
DR WormPep; K02A2.6; CE02792.
DR InterPro; IPR009007; Pept_A_acid.
DR InterPro; IPR001584; Rve.
DR InterPro; IPR000477; RVTse.
DR InterPro; IPR001876; Znf_CCHC.
DR Pfam; PF00665; rve; 1.
DR Pfam; PF00078; rvt; 1.
DR Pfam; PF00098; zf-CCHC; 1.
DR PRINTS; PR00939; C2HCZNFINGER.
DR SMART; SMO0343; Znf_C2HC; 1.

DR PROSITE: PS50158; 2F CCHC; 1.
KW Hypothetical protein; Zinc-finger.
FT ZN_FING 239 256 CCHC-TYPE.
SQ SEQUENCE 1268 AA; 143493 MW; AACAC4235AAE468 CRC64;
Query Match 63.2%; Score 36; DB 1; Length 1268;
Best Local Similarity 50.0%; Pred. No. 56;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1 KKQYTSIHGG 10
:|:|:||||
Db 1043 QKYYVQVHHG 1052
Search completed: October 4, 2004, 18:57:07
Job time : 10.2609 secs

OM protein - protein search, using sw model

Run on: October 4, 2004, 18:37:37 ; Search time 47.3913 Seconds
(without alignments)
66.577 Million cell updates/sec

Title: US-10-048-209-3

Perfect score: 57

Sequence: 1 KKQYTSIHNG 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_phc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	Score	Match	Length	DB	ID	Description
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RESULT 1	
ID	O97917
AC	O97917
DT	01-MAY-1999 (TrEMBLrel. 10, Created)
DT	01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT	01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

ALIGNMENTS

1	57	100.0	49	6	O97917	O97917 bos taurus
2	57	100.0	113	13	Q8JH58	Q8JH58 chelydra se
3	57	100.0	218	11	Q8EPV5	Q8EPV5 mus musculus
4	57	100.0	239	13	Q8UUI7	Q8UUI7 brachydanio
5	57	100.0	357	13	Q8UUI8	Q8UUI8 brachydanio
6	57	100.0	384	11	Q8BPC7	Q8BPC7 mus musculus
7	57	100.0	472	13	Q8UUS0	Q8UUS0 brachydanio
8	57	100.0	534	13	Q93296	Q93296 gallus gall
9	57	100.0	569	13	Q9PYL1	Q9PYL1 gallus gall
10	57	100.0	612	13	Q919E7	Q919E7 brachydanio
11	57	100.0	678	13	Q7ZT11	Q7ZT11 brachydanio
12	57	100.0	694	13	Q8UUR9	Q8UUR9 brachydanio
13	57	100.0	695	13	Q9DGJ8	Q9DGJ8 gallus gall
14	57	100.0	699	13	Q57394	Q57394 narke japon
15	57	100.0	738	13	Q90W28	Q90W28 brachydanio
16	57	100.0	751	13	Q9DGJ7	Q9DGJ7 gallus gall
17	54	94.7	693	13	Q98SG0	Q98SG0 xenopus lae
18	54	94.7	695	13	Q98SF9	Q98SF9 xenopus lae
19	54	94.7	695	13	Q7ZXQ0	Q7ZXQ0 xenopus lae
20	54	94.7	747	13	Q91963	Q91963 xenopus. ap
21	50	87.7	82	4	Q16020	Q16020 homo sapien
22	50	87.7	82	4	Q16014	Q16014 homo sapien
23	50	87.7	82	4	Q16019	Q16019 homo sapien
24	42	73.7	133	5	O17443	O17443 brevicosyne
25	38	66.7	228	16	Q8AOP0	Q8AOP0 bacteroides
26	38	66.7	289	16	Q8RII2	Q8RII2 fusobacteri
27	37	64.9	164	16	Q81P90	Q81P90 bacillus an
28	37	64.9	442	16	Q92AT6	Q92AT6 listeria in
29	37	64.9	2584	5	Q9TW88	Q9TW88 caenorhabdi
30	37	64.9	2606	5	Q21920	Q21920 caenorhabdi
31	36	63.2	71	16	Q83DX8	Q83DX8 coxiella bu
32	36	63.2	116	11	Q8CE5	Q8CE5 mus musculus
33	36	63.2	159	17	Q8TTR5	Q8TTR5 methanosarc
34	36	63.2	159	17	Q8TTR3	Q8TTR3 methanosarc
35	36	63.2	275	16	Q9RXF2	Q9RXF2 deinococcus
36	36	63.2	333	13	Q90YZ9	Q90YZ9 sphyraena i
37	36	63.2	412	5	Q21806	Q21806 caenorhabdi
38	36	63.2	443	2	Q9ZA32	Q9ZA32 streptomyce
39	36	63.2	464	10	Q9FEP0	Q9FEP0 adonis pala
40	36	63.2	550	8	Q7IAJ6	Q7IAJ6 chara vulga
41	36	63.2	729	16	Q8DKG0	Q8DKG0 synechococo
42	36	63.2	904	10	Q9SF47	Q9SF47 arabidopsis
43	36	63.2	944	5	Q8T4F6	Q8T4F6 drosophila
44	36	63.2	944	5	Q9VK06	Q9VK06 drosophila
45	36	63.2	1313	5	P91422	P91422 caenorhabdi

DE Amyloid protein (Fragment).

GN APP.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RK MEDLINE=20063685; PubMed=10594237;
RA Konfortov B.A., Licence V.E., Miller J.R.;
RT "Resequencing of DNA from a diverse panel of cattle reveals a high
RT level of polymorphism in both intron and exon.";
RL Mamm. Genome 10:1142-1145(1999).
DR EMBL; AJ133033; CAB38017.1; -.
DR HSSP; P05067; 1BA4
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF03494; Beta-APP; 1.
FT NON_TER 1
FT NON_TER 49
SQ SEQUENCE 49 AA; 5183 MW; 6287463F0559BDE CRC64;

Query Match 100.0%; Score 57; DB 6; Length 49;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKQYTSIHGG 10
Db 37 KKQYTSIHGG 46

RESULT 2

Q8JH58 ID Q8JH58 PRELIMINARY; PRT; 113 AA.
AC Q8JH58;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Amyloid beta protein (fragment).
OS Chelydra serpentina serpentina (common snapping turtle).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Testudines; Cryptodira; Testudinoidea; Chelydridae; Chelydra.
OX NCBI_TaxID=134619;
RN [1]
RP SEQUENCE FROM N.A.
RK MEDLINE=21876906; PubMed=11882478;
RA Trudeau V.L., Chiu S., Kennedy S.W., Brooks R.J.;
RT "Octylphenol (OP) alters the expression of members of the amyloid
RT protein family in the hypothalamus of the snapping turtle, Chelydra
RT serpentina serpentina.";
RL Environ. Health Perspect. 110:269-275(2002).
DR EMBL; AF541917; AAN04308.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR008155; A4_APP.
DR Pfam; PF03494; Beta-APP; 1.
DR

DR PRINTS; PR00203; AMYLOIDA4.
DR PROSITE; PS00320; A4_INTRA; 1.
FT NON_TER 1
SQ SEQUENCE 113 AA; 12750 MW; 72515C930496E053 CRC64;

Query Match 100.0%; Score 57; DB 13; Length 113;
Best Local Similarity 100.0%; Pred. No. 0.0042;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKQYTSIHGG 10
Db 68 KKQYTSIHGG 77

RESULT 3

Q8BPV5 ID Q8BPV5 PRELIMINARY; PRT; 218 AA.
AC Q8BPV5;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Amyloid beta (fragment).
GN APP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK052448; BAC34997.1; -.
DR MGD; MGI:88059; App.
DR GO; GO:000515; P:protein binding; IPI.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PROSITE; PS00320; A4_INTRA; 1.
FT NON_TER 1
SQ SEQUENCE 218 AA; 24118 MW; 95B55AFDAE1D0EF5 CRC64;

Query Match 100.0%; Score 57; DB 11; Length 218;
Best Local Similarity 100.0%; Pred. No. 0.0082;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKQYTSIHGG 10
Db 173 KKQYTSIHGG 182

RESULT 4


```

RC TISSUE=Embryo;
RX PubMed=11862463;
RX Musa A., Lehrach H., Russo V.E.A.;
RRT "distinct expression patterns of two zebrafish homologues of the human
RRT APP gene during embryonic development.";
RRL Dev. Genes Evol. 211:563-567(2001).
RRL ENBL; AJ315637; CAC85734.1; -.
DR 2FIN; ZDR-GENE-000616-13; appa.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPRO08155; A4_APP.
DR InterPro; IPRO01255; Beta-APP.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PROSITE; PS00320; A4_INTRA; 1.
DR NON_TER 1
SQ SEQUENCE 357 AA; 49662 MW; 07D998EF6C55B2D8 CRC64;

Query Match 100.0%; Score 57; DB 13; Length 357;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKYQTSIHGG 10
   | | | | | | | |
Do 312 KKYQTSIHGG 321

RESULT 6
QB8PC7 PRELIMINARY; PRT; 384 AA.
ID QB8PC7
AC QB8PC7;
DT 01-VAR-2003 (tREMBLrel. 23, Created)
DT 01-VAR-2003 (tREMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (tREMBLrel. 25, Last annotation update)
DE Amyloid beta (Fragment).
DE App.
GN GN
OS Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxId=10090;
[1] RN
RNP SEQUENCE FROM N.A.
RRC STRAIN=C57BL/6J; TISSUE=Head;
RRC MEDLINE=22354683; PubMed=1246681;
RX The FANTOM Consortium,
RRT the RIKEN Genome Exploration Research Group Phase I & II Team;
RRT "Analysis of the mouse transcriptome based on functional annotation of
RRL 60,770 full-length cDNAs.";
RRL Nature 420:563-573(2002).
DR ENBL; AK076506; BAC36369.1; -.
DR MGD; MGI:88059; App.
DR GO; GO:0005515; F:protein binding; IPI.
DR InterPro; IPRO08155; A4_APP.
DR InterPro; IPRO01255; Beta-APP.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PROSITE; PS00320; A4_INTRA; 1.
DR NON_TER 1
FT NON_TER 1

```

SQ SEQUENCE 384 AA; 43990 MW; A81B1AD8AE683173 CRC64;
 Query Match 100.0%; Score 57; DB 11; Length 384;
 Best Local Similarity 100.0%; Pred. No. 0.015; 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0;
 QY 1 KQYTSIHGG 10
 |||||
 DB 339 KQYTSIHGG 348
 |||||
 RESULT 7
 Q8U50 PRELIMINARY; PRT; 472 AA.
 ID Q8U50;
 AC Q8U50;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Putative membrane protein (Fragment).
 GN APPA.
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX PubMed=11862463;
 RA Musa A., Lehrach H., Russo V.E.A.;
 RT "Distinct expression patterns of two zebrafish homologues of the human
 RT APP gene during embryonic development."
 RL Dev. Genes Evol. 211:563-567(2001).
 DR EMBL; AJ315636; CAC85733.1; -.
 DR ZFIN; ZDB-GENE-000616-13; appa.
 DR GO; GO:0016020; C:membrane; IEA.
 DR InterPro; IPR008155; A4_APP.
 DR InterPro; IPR001255; Beta-APP.
 DR Pfam; PFO3494; Beta-APP; 1.
 DR PRINTS; PR00203; AMYLOIDA.
 DR PROSITE; PS00320; A4_INTRA; 1.
 DR NON_TER 1
 FT SEQUENCE 472 AA; 53787 MW; 24F7128BE3356550 CRC64;
 Query Match 100.0%; Score 57; DB 13; Length 472;
 Best Local Similarity 100.0%; Pred. No. 0.018; 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0;
 QY 1 KQYTSIHGG 10
 |||||
 DB 427 KQYTSIHGG 436
 |||||
 RESULT 8
 Q93296 PRELIMINARY; PRT; 534 AA.
 ID Q93296
 AC Q93296;
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Amyloid protein (Fragment).
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=98337885; PubMed=9671674;
 RA Barnes N.Y., Li L., Yoshikawa K., Schwartz L.M., Oppenheim R.W.,
 RA Milligan C.E.;
 RT "Increased production of amyloid precursor protein provides a
 RT substrate for caspase-3 in dying motoneurons."
 RL J. Neurosci. 18:5869-5880(1998).
 DR EMBL; AF042098; AAC25052.1; -.
 DR HSP; P05067; 1BA4.
 DR GO; GO:0016020; C:membrane; IEA.
 DR InterPro; IPR008155; A4_APP.
 DR InterPro; IPR001255; Beta-APP.
 DR Pfam; PFO2177; A4_EXTRA; 1.
 DR Pfam; PFO3494; Beta-APP; 1.
 DR PRINTS; PR00203; AMYLOIDA.
 DR PROSITE; PS00319; A4_EXTRA; 1.
 DR PROSITE; PS00320; A4_INTRA; 1.
 DR NON_TER 1
 FT SEQUENCE 534 AA; 60597 MW; FB53ECC2E66D4C92 CRC64;
 Query Match 100.0%; Score 57; DB 13; Length 534;
 Best Local Similarity 100.0%; Pred. No. 0.021; 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0;
 QY 1 KQYTSIHGG 10
 |||||
 DB 489 KQYTSIHGG 498
 |||||
 RESULT 9
 Q9PVL1 PRELIMINARY; PRT; 569 AA.
 ID Q9PVL1
 AC Q9PVL1;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Amyloid protein (Fragment).
 GN APP.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;

RA Coulson E.J., Paliga K., Beyreuther K., Masters C.L.;
RT "What the evolution of the amyloid protein precursor supergene family
RL Neurochem Int. 0:0-0(2000).";
DR EMBL; AF030341; AA12698.1; -.
DR HSSP; P05067; IEA4.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR008154; A4_extra.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
FT NON_TER 1
SQ SEQUENCE 569 AA; 64753 MW; 0ABEBB851863A19D CRC64;
Query Match 100.0%; Score 57; DB 13; Length 569;
Best Local Similarity 100.0%; Pred. No. 0.022; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKQYTSIHG 10
| | | | | | | | | |
DB 525 KKQYTSIHG 534

RESULT 10
Q919E7
ID Q919E7 PRELIMINARY; PRT; 612 AA.
AC Q919E7;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Amyloid protein (Fragment).
GN APPA.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Slavov D.B., Gardiner K.;
RT "An App cDNA from Zebrafish (Danio rerio).";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF257742; AA71748.1; -.
DR HSSP; P05067; 1H23.
DR ZFIN; ZDB-GENE-000616-13; appa.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR008154; A4_extra.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.

DR PROSITE; PS00320; A4_INTRA; 1.
FT NON_TER 1
SQ SEQUENCE 612 AA; 69710 MW; 59A9ACBDF9C59EFF CRC64;
Query Match 100.0%; Score 57; DB 13; Length 612;
Best Local Similarity 100.0%; Pred. No. 0.024; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKQYTSIHG 10
| | | | | | | | | |
DB 567 KKQYTSIHG 576

RESULT 11
Q7ZZT1
ID Q7ZZT1 PRELIMINARY; PRT; 678 AA.
AC Q7ZZT1;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Amyloid protein a variant 2.
GN APPA.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Groth C., Lardelli M.;
RT "Investigation of zebrafish appa expression during embryogenesis.";
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY271746; AAP22958.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR001255; Beta-APP.
DR InterPro; IPR008154; A4_extra.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR SMART; SM00006; A4_EXTRA; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
SQ SEQUENCE 678 AA; 76755 MW; 94163778444FD0BC CRC64;
Query Match 100.0%; Score 57; DB 13; Length 678;
Best Local Similarity 100.0%; Pred. No. 0.026; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKQYTSIHG 10
| | | | | | | | | |
DB 633 KKQYTSIHG 642

RESULT 12
Q8UUR9
ID Q8UUR9 PRELIMINARY; PRT; 694 AA.

AC Q9UURS; Sarasa M., Rodolase A., Sortibas V.;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Putative membrane protein.
 GN APPB.
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX PubMed=11862463;
 RA Musa A., Lebrach H., Russo V.E.A.;
 RT "Distinct expression patterns of two zebrafish homologues of the human
 RL Dev. Genes Evol. 211:563-567(2001).
 DR EMBL; AJ315639; CAC85736.1; -.
 DR ZFIN; ZDB-GENE-020220-1; appb.
 DR GO; GO:0016020; C:membrane; IEA.
 DR InterPro; IPR008155; A4_APP.
 DR InterPro; IPR008154; A4_extra.
 DR Pfam; PF02177; A4_EXTRA; 1.
 DR Pfam; PF03494; Beta-APP; 1.
 DR PRINTS; PR00203; AMYLOIDA4.
 DR SMART; SM00006; A4_EXTRA; 1.
 DR PROSITE; PS00319; A4_EXTRA; 1.
 DR PROSITE; PS00320; A4_INTRA; 1.
 SQ SEQUENCE 694 AA; 75228 MW; 2B03382D411162DC CRC64;
 Query Match 100.0%; Score 57; DB 13; Length 694;
 Best Local Similarity 100.0%; Pred. No. 0.027;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KQYTSIHGG 10
 Db 649 KQYTSIHGG 658
 RESULT 13
 Q9DGSB PRELIMINARY; PRT; 695 AA.
 AC Q9DGSB;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Beta-amyloid precursor protein 695 isoform.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.

RA Sarasa M., Rodolase A., Sortibas V.;
 RT "Cloning of full-length chicken beta-amyloid precursor protein
 RI isoforms."
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF289218; AAG00593.1; -.
 DR HSSP; P05067; 1BA4.
 DR GO; GO:0016020; C:membrane; IEA.
 DR InterPro; IPR008155; A4_APP.
 DR InterPro; IPR008154; A4_extra.
 DR InterPro; IPR001255; Beta-APP.
 DR Pfam; PF02177; A4_EXTRA; 1.
 DR Pfam; PF03494; Beta-APP; 1.
 DR PRINTS; PR00203; AMYLOIDA4.
 DR SMART; SM00006; A4_EXTRA; 1.
 DR PROSITE; PS00319; A4_EXTRA; 1.
 DR PROSITE; PS00320; A4_INTRA; 1.
 SQ SEQUENCE 695 AA; 75565 MW; F201EDQ2AEC86D95 CRC64;
 Query Match 100.0%; Score 57; DB 13; Length 695;
 Best Local Similarity 100.0%; Pred. No. 0.027;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KQYTSIHGG 10
 Db 650 KQYTSIHGG 659
 RESULT 14
 Q57394 PRELIMINARY; PRT; 699 AA.
 AC Q57394;
 DT 01-JUN-1998 (TrEMBLrel. 06, Created)
 DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE EL amyloid precursor protein 699.
 GN EL APP699.
 OS Narke japonica (Electric ray).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
 OC Elasmobranchii; Squalia; Hymnosqualea; Pristigaster; Batoidae;
 OC Torpediniformes; Narcinoidae; Narkidae; Narke.
 OX NCBI_TaxID=62965;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Electric lobe;
 RX MEDLINE=98129705; PubMed=9461486;
 RA Iijima K., Lee D.-S., Okutsu J., Tomita S., Hirashima N., Kirino Y.,
 RA Suzuki T.;
 RT "cDNA isolation of Alzheimer's amyloid precursor protein from
 RT cholinergic nerve terminals of the electric organ of the electric
 RL Biochem. J. 330:29-33(1998).
 DR EMBL; AB005544; BAA24230.1; -.
 DR HSSP; P05067; 1H23.
 DR GO; GO:0016020; C:membrane; IEA.
 DR InterPro; IPR008155; A4_APP.
 DR InterPro; IPR008154; A4_extra.
 DR InterPro; IPR001255; Beta-APP.

DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PS00203; AMYLOIDA4.
DR SMART; SMO0006; A4_EXTRA; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
SQ SEQUENCE 699 AA; 78879 MW; 952915C309D50E5C CRC64;
Query Match 100.0%; Score 57; DB 13; Length 699;
Best Local Similarity 100.0%; Pred.No. 0.027;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KQYTSIHG 10
Db 654 KQYTSIHG 663

RESULT 15
ID Q90W28 PRELIMINARY; PRT; 738 AA.
AC Q90W28;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Amyloid precursor protein.
GN APPA OR APP.
OS Brachydanio rerio (zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Groth C., Lardelli M.;
RT "Expression analysis of zebrafish app.";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF389401; AAK64495.1; -.
DR ZFIN; ZDB-GENE-000616-13; appa.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004867; F:serine protease inhibitor activity; IEA.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR008154; A4_extra.
DR InterPro; IPR001255; Beta-APP.
DR InterPro; IPR002223; Kunitz_BPTI.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PS00203; AMYLOIDA4.
DR PRINTS; PS00759; BASICPTASE.
DR ProDom; PD000222; Kunitz_BPTI; 1.
DR SMART; SMO0006; A4_EXTRA; 1.
DR SMART; SMO0131; KU; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 1.
KW Protease inhibitor; Serine protease inhibitor.

SQ SEQUENCE 738 AA; 83577 MW; AF480F6D308FD298 CRC64;
Query Match 100.0%; Score 57; DB 13; Length 738;
Best Local Similarity 100.0%; Pred.No. 0.029;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KQYTSIHG 10
Db 693 KQYTSIHG 702
Search completed: October 4, 2004, 18:56:22
Job time : 48.3913 secs

OM protein - protein search, using sw model

Run on: October 4, 2004, 18:37:13 ; Search time 63.8478 Seconds
(without alignments)
48.679 Million cell updates/sec

Title: US-10-048-209-4
Perfect score: 62
Sequence: 1 KKQYTSIHG 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547305 residues
Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04: +
1: geneseqp1980s: +
2: geneseqp1990s: +
3: geneseqp2000s: +
4: geneseqp2001s: +
5: geneseqp2002s: +
6: geneseqp2003as: +
7: geneseqp2003bs: +
8: geneseqp2004s: +

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	62	100.0	13	4 AAB67794	Aab67794 Cytoplasm
2	62	100.0	15	4 AAB67798	Aab67798 Cytoplasm
3	62	100.0	19	7 ADC49255	Adc49255 Human inh
4	62	100.0	32	6 AAC19883	Aac19883 Human amy
5	62	100.0	33	7 ADC49254	Adc49254 Human inh
6	62	100.0	41	4 AAM16658	Aam16658 Peptide #
7	62	100.0	41	4 ABB35642	Abb35642 Peptide #
8	62	100.0	41	4 AAM29142	Aam29142 Peptide #
9	62	100.0	41	4 ABB30475	Abb30475 Peptide #

10	62	100.0	41	4 ABB21071	Abb21071 Protein #
11	62	100.0	41	4 AAM56458	Aam56458 Human bra
12	62	100.0	41	4 AAM04374	Aam04374 Peptide #
13	62	100.0	41	5 ABC38416	Abg38416 Human pep
14	62	100.0	44	2 AAM53985	Aam53985 Human ALZ
15	62	100.0	47	2 AAR58917	Aar58917 Cytoplasm
16	62	100.0	47	2 AAW26395	Aaw26395 Amyloid p
17	62	100.0	47	2 AAW26402	Aaw26402 Amyloid p
18	62	100.0	47	2 AAW26400	Aaw26400 Amyloid p
19	62	100.0	47	2 AAW26403	Aaw26403 Amyloid p
20	62	100.0	47	2 AAW26399	Aaw26399 Amyloid p
21	62	100.0	47	2 AAW26401	Aaw26401 Amyloid p
22	62	100.0	47	2 AAW26520	Aaw26520 Amyloid p
23	62	100.0	47	2 AAW26518	Aaw26518 Amyloid p
24	62	100.0	47	2 AAW26521	Aaw26521 Amyloid p
25	62	100.0	47	2 AAW26519	Aaw26519 Amyloid p
26	62	100.0	47	2 AAW26513	Aaw26513 Amyloid p
27	62	100.0	47	2 AAW26517	Aaw26517 Amyloid p
28	62	100.0	47	2 AAW42984	Aaw42984 APP isofo
29	62	100.0	47	2 AAW42986	Aaw42986 APP isofo
30	62	100.0	47	2 AAW42987	Aaw42987 APP isofo
31	62	100.0	47	2 AAW42983	Aaw42983 APP isofo
32	62	100.0	47	2 AAW42985	Aaw42985 APP isofo
33	62	100.0	47	2 AAW4755	Aaw4755 APP-REP 7
34	62	100.0	47	2 AAW4753	Aaw4753 APP-REP 7
35	62	100.0	47	2 AAW4749	Aaw4749 APP-REP 7
36	62	100.0	47	2 AAW4756	Aaw4756 APP-REP 7
37	62	100.0	47	2 AAW4754	Aaw4754 APP-REP 7
38	62	100.0	47	2 AAW4757	Aaw4757 APP-REP 7
39	62	100.0	47	2 AAW4274	Aaw4274 Amyloid p
40	62	100.0	47	4 AAB67791	Aab67791 Cytoplasm
41	62	100.0	47	7 ADC49250	Adc49250 Human inh
42	62	100.0	47	7 ADC49249	Adc49249 Inhibitor
43	62	100.0	47	7 ADC49251	Adc49251 Human inh
44	62	100.0	49	2 AAR35087	Aar35087 Human amy
45	62	100.0	49	4 AAM14458	Aam14458 Peptide #

ALIGNMENTS

RESULT 1
AAB67794
ID AAB67794 standard; peptide; 13 AA.
XX
AC AAB67794;
XX
DT 11-JUN-2001 (first entry)
XX

Cytoplasmic domain of the amyloid protein precursor (APP).
XX Amyloid protein precursor; APP; apoptosis; cancer; Alzheimer's disease.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 1

FT /note= "this residue represents an internalisation
 FT peptide such as the sequence given in AAB67795"
 FT Misc-difference 13
 FT /note= "this residue represents V, VV, VF, VWF, VWEV, VWEVD"
 XX
 XX WO200109170-A1.
 XX
 XX 08-FEB-2001.
 XX
 XX 28-JUL-2000; 2000WO-FR002174.
 XX
 XX 30-JUL-1999; 99FR-00009929.
 XX
 XX (CNRS) CNRS CENT NAT RECH SCI.
 XX
 XX Allinquant B, Prochiantz A;
 XX WPI; 2001-257398/26.
 XX
 XX Peptides derived from the cytoplasmic domain of the amyloid protein
 XX precursor, useful in the treatment of cancer and Alzheimer's disease.
 XX
 XX Claim 1; Page 13; 28pp; French.
 XX
 XX The present sequence represents a peptide derived from the cytoplasmic
 XX domain of the human amyloid protein precursor (APP). APP peptides derived
 XX from the cytoplasmic domain, and containing the membrane domain
 XX juxtaposed to the cytoplasmic domain of APP are useful for selecting and
 XX screening products capable of inhibiting apoptosis. The peptides are
 XX useful in the treatment of cancer and Alzheimer's disease
 XX
 XX Sequence 13 AA;
 SQ Query Match 100.0%; Score 62; DB 4; Length 13;
 Best Local Similarity 100.0%; Pred. No. 0.00019;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KKKQYTSIHG 11
 Db 2 KKKQYTSIHG 12
 RESULT 2
 AAB67798
 ID AAB67798 standard; peptide; 15 AA.
 XX
 XX AC AAB67798;
 XX
 XX DT 11-JUN-2001 (first entry)
 XX
 XX DE Cytoplasmic domain of the amyloid protein precursor (APP).
 XX
 XX KW Amyloid protein precursor; APP; apoptosis; cancer; Alzheimer's disease.
 XX
 XX OS Homo sapiens.
 XX
 XX PF WO200109170-A1.
 XX

XX 08-FEB-2001.
 PD
 XX
 XX 28-JUL-2000; 2000WO-FR002174.
 XX
 XX 30-JUL-1999; 99FR-00009929.
 XX
 XX (CNRS) CNRS CENT NAT RECH SCI.
 XX
 XX Allinquant B, Prochiantz A;
 XX WPI; 2001-257398/26.
 XX
 XX Peptides derived from the cytoplasmic domain of the amyloid protein
 XX precursor, useful in the treatment of cancer and Alzheimer's disease.
 XX
 XX Disclosure; Page 2; 28pp; French.
 XX
 XX The present sequence represents a peptide derived from the cytoplasmic
 XX domain of the human amyloid protein precursor (APP). APP peptides derived
 XX from the cytoplasmic domain, and containing the membrane domain
 XX juxtaposed to the cytoplasmic domain of APP are useful for selecting and
 XX screening products capable of inhibiting apoptosis. The peptides are
 XX useful in the treatment of cancer and Alzheimer's disease
 XX
 XX Sequence 15 AA;
 SQ Query Match 100.0%; Score 62; DB 4; Length 15;
 Best Local Similarity 100.0%; Pred. No. 0.00022;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KKKQYTSIHG 11
 Db 1 KKKQYTSIHG 11
 RESULT 3
 ADC49255
 ID ADC49255 standard; protein; 19 AA.
 XX
 XX AC ADC49255;
 XX
 XX DT 18-DEC-2003 (first entry)
 XX
 XX DE Human inhibitor of metabolic degradation of APP variant #4.
 XX
 XX KW human; inhibitory factor; metabolic degradation of APP;
 KW amyloid precursor protein; Alzheimer's disease; mutant; mutein.
 XX
 XX OS Homo sapiens.
 XX
 XX PN JP2002360252-A.
 XX
 XX PD 17-DEC-2002.
 XX
 XX PF 27-APR-2001; 2001JP-00133178.
 XX

PR 27-APR-2001; 2001JP-00133178.
 XX (SUZU/) SUZUKI T.
 PA (SUMU) SUMITOMO SEIYAKU KK.
 XX WPI; 2003-516151/49.
 DR
 XX An inhibitory factor of metabolic degradation of amyloid precursor
 PT protein (APP) which inhibits formation of beta-amyloid, useful in the
 PT treatment of Alzheimer's disease.
 XX
 PS Disclosure; SEQ ID NO 15; 33pp; Japanese.
 CC The invention relates to an inhibitory factor of metabolic degradation of
 CC APP. The factor is useful in the treatment of Alzheimer's disease. The
 CC present sequence is used in the exemplification of the invention.
 XX
 SQ Sequence 19 AA;
 Query Match 100.0%; Score 62; DB 7; Length 19;
 Best Local Similarity 100.0%; Pred. No. 0.00029;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KKKQYTSIHG 11
 Db 1 KKKQYTSIHG 11
 RESULT 4
 AAO19863
 ID AAO19863 standard; peptide; 32 AA.
 XX AC AAO19863;
 XX 11-AUG-2003 (first entry)
 XX Human amyloid precursor protein APP immunogenic peptide #3.
 XX Human; APP; amyloid precursor protein; immunogen; Alzheimer's disease;
 KW high-throughput screening; neuroprotective; nootropic; antiparkinsonian.
 XX Homo sapiens.
 OS WO2003001881-A2.
 PN 09-JAN-2003.
 XX 26-JUN-2002; 2002WO-US020267.
 PF 26-JUN-2001; 2001US-0300959P.
 XX (NYME-) NEW YORK STATE OFFICE MENTAL HEALTH.
 PA Mathews PM, Nixon RA, Schmidt SD, Jiang Y;
 PI WPI; 2003-210182/20.
 XX

PT Identifying compounds that modulates the generation of metabolites
 PT associated with a disease or disorder, for treating e.g. Alzheimer's
 PT disease by determining levels of a cellular component protein, or its
 PT conformation state.
 XX
 PS Example 1; Page 29; 69pp; English.
 XX
 CC The present-invention relates to a method of identifying compounds that
 CC modulate the generation of one or more metabolites associated with a
 CC disease or disorder comprising determining levels of a cellular component
 CC protein or a conformation state of a cellular precursor protein. In
 CC particular, the method can be used to determine levels of amyloid
 CC precursor protein (APP), which is associated with Alzheimer's disease. It
 CC is also useful for identifying compounds as drugs for treating diseases
 CC or disorders associated with metabolic and/or proteolytic pathways, e.g.
 CC Alzheimer's disease, Parkinson's disease, Huntington's disease, lysosomal
 CC storage disorders, prion diseases, the tau-based neurodegenerative
 CC disorders, and other non-AD amyloidoses. The present sequence is an
 CC immunogenic portion of human APP
 XX
 SQ Sequence 32 AA;
 Query Match 100.0%; Score 62; DB 6; Length 32;
 Best Local Similarity 100.0%; Pred. No. 0.00051;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KKKQYTSIHG 11
 Db 5 KKKQYTSIHG 15
 RESULT 5
 ADC49254
 ID ADC49254 standard; protein; 33 AA.
 XX AC ADC49254;
 XX 18-DEC-2003 (first entry)
 XX Human inhibitor of metabolic degradation of APP variant #3.
 XX human; inhibitory factor; metabolic degradation of APP;
 KW amyloid precursor protein; Alzheimer's disease; mutant; mutein.
 XX Homo sapiens.
 OS JP2002360252-A.
 PN 17-DEC-2002.
 PD 27-APR-2001; 2001JP-00133178.
 PF 27-APR-2001; 2001JP-00133178.
 XX (SUZU/) SUZUKI T.
 PA (SUMU) SUMITOMO SEIYAKU KK.
 XX

DR WPI; 2003-516151/49.

XX An inhibitory factor of metabolic degradation of amyloid precursor

PT protein (APP) which inhibits formation of beta-amyloid, useful in the

PT treatment of Alzheimer's disease.

XX

XX Disclosure; SEQ ID NO 14; 33pp; Japanese.

PS

CC The invention relates to an inhibitory factor of metabolic degradation of

CC APP. The factor is useful in the treatment of Alzheimer's disease. The

CC present sequence is used in the exemplification of the invention.

XX

XX Sequence 33 AA;

QY Query Match 100.0%; Score 62; DB 7; Length 33;

Best Local Similarity 100.0%; Pred. No. 0.00053;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKKQYTSIHG 11

Db 1 KKKQYTSIHG 11

RESULT 6

AAM16658

ID AAM16658 standard; protein; 41 AA.

XX

XX AAM16658;

DT 12-OCT-2001 (first entry)

DE Peptide #3092 encoded by probe for measuring cervical gene expression.

XX

XX Probe; human; microarray; gene expression; cervical epithelial cell;

XX cervical cancer.

XX Homo sapiens.

OS

XX W0200157278-A2.

PN

XX 09-AUG-2001.

PD

XX 30-JAN-2001; 2001WO-US000670.

PF

XX 04-FEB-2000; 2000US-0180312P.

PR 26-MAY-2000; 2000US-0207456P.

PR 30-JUN-2000; 2000US-00608408.

PR 03-AUG-2000; 2000US-00632366.

PR 21-SEP-2000; 2000US-0234687P.

PR 27-SEP-2000; 2000US-0236359P.

PR 04-OCT-2000; 2000GB-00024263.

XX

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-488901/53.

DR

XX Human genome-derived single exon nucleic acid probes useful for analyzing

PT gene expression in human cervical epithelial cells.

XX

XX Claim 27; SEQ ID NO 21484; 487pp; English.

XX

CC The present invention relates to human single exon nucleic acid probes

CC (SENPs: see A110068-A128459). The present sequence is a peptide encoded

CC by one such probe. The SENPs are derived from human HeLa cells. The SENPs

CC can be used to produce a single exon microarray, which can be used for

CC measuring human gene expression in a sample derived from human cervical

CC epithelial cells. By measuring gene expression, the probes are therefore

CC useful in grading and/or staging of diseases of the cervix, notably

CC cervical cancer. Note: The sequence data for this patent did not form

CC part of the printed specification, but was obtained in electronic format

CC directly from WIPO at ftp.wipo.int/pub/published_pot_sequences

XX

XX Sequence 41 AA;

QY 1 KKKQYTSIHG 11

Db 28 KKKQYTSIHG 38

RESULT 7

ABB35642

ID ABB35642 standard; peptide; 41 AA.

XX

XX ABB35642;

AC

XX 04-FEB-2002 (first entry)

DT

XX Peptide #3148 encoded by human foetal liver single exon probe.

DE

XX Human; foetal liver; gene expression; single exon nucleic acid probe.

KW

XX Homo sapiens.

OS

XX W0200157277-A2.

PN

XX 09-AUG-2001.

PD

XX 30-JAN-2001; 2001WO-US000669.

PF

XX 04-FEB-2000; 2000US-0180312P.

PR 26-MAY-2000; 2000US-0207456P.

PR 30-JUN-2000; 2000US-00608408.

PR 03-AUG-2000; 2000US-00632366.

PR 21-SEP-2000; 2000US-0234687P.

PR 27-SEP-2000; 2000US-0236359P.

PR 04-OCT-2000; 2000GB-00024263.

XX

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;
PI WPI; 2001-483447/52.
XX Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human fetal liver.
XX Claim 27; SEQ ID NO 28277; 639pp + Sequence Listing; English.
XX The invention relates to a single exon nucleic acid probe for measuring
CC human gene expression in a sample derived from human foetal liver. The
CC single exon nucleic acid probes may be used for predicting, measuring and
CC displaying gene expression in samples derived from human fetal liver. The
CC present sequence is a peptide encoded by a single exon nucleic acid probe
CC of the invention. Note: The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pat_sequences
XX
SQ Sequence 41 AA;

Query Match 100.0%; Score 62; DB 4; Length 41;
Best Local Similarity 100.0%; Pred. No. 0.00067; Mismatches 0; Indels 0; Gaps 0;
Matches 11; Conservative 0;

QY 1 KKKQYTSIHG 11
| | | | | | | | | |
Db 28 KKKQYTSIHG 38

RESULT 8
AM29142
ID AM29142 standard; protein; 41 AA.
XX
AC AM29142;
XX
DT 17-OCT-2001 (first entry)
XX
DE Peptide #3179 encoded by probe for measuring placental gene expression.
XX
KW Probe; microarray; human; placenta; antenatal diagnosis;
KW genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200157272-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000663.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.

PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-488897/53.
XX
PT Human genome-derived single exon nucleic acid probes useful for analyzing
PI gene expression in human placenta.
XX
PS Claim 27; SEQ ID NO 29411; 654pp; English.
XX
CC The present invention relates to single exon nucleic acid probes (SENP:
CC see AAI31315-AAI57546). The present sequence is a peptide encoded by one
CC such probe. The probes are useful for producing a microarray for
CC predicting, measuring and displaying gene expression in samples derived
CC from human placenta. The probes are useful for antenatal diagnosis of
CC human genetic disorders
XX
SQ Sequence 41 AA;

Query Match 100.0%; Score 62; DB 4; Length 41;
Best Local Similarity 100.0%; Pred. No. 0.00067; Mismatches 0; Indels 0; Gaps 0;
Matches 11; Conservative 0;

QY 1 KKKQYTSIHG 11
| | | | | | | | | |
Db 28 KKKQYTSIHG 38

RESULT 9
ABB30475
ID ABB30475 standard; peptide; 41 AA.
XX
AC ABB30475;
XX
DT 01-FEB-2002 (first entry)
XX
DE Peptide #3126 encoded by breast cell single exon nucleic acid probe.
XX
KW Human; microarray; single exon probe; gene expression; breast; disease;
KW cancer.
XX
OS Homo sapiens.
XX
PN WO200157271-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000662.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.

PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 PA PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX WPI; 2001-496933/54.
 XX New spatially-addressable set of single exon nucleic acid probes, useful
 PT for measuring gene expression in sample derived from human breast,
 PT comprises number of single exon nucleic acid probes.
 XX Claim 27; SEQ ID NO 13443; 327bp + Sequence Listing; English.
 XX The invention relates to a spatially-addressable set of single exon
 CC nucleic acid probes for measuring gene expression in a sample derived
 CC from human breast and BT 474 cells. The method involves contacting the
 CC probes with a collection of detectably labelled nucleic acids derived
 CC from mRNA of human breast, and then measuring the label bound to each
 CC probe of the microarray. The probes are useful for verifying the
 CC expression of regions of genomic DNA predicted to encode proteins. They
 CC are useful for gene discovery, and for determining predisposition and/or
 CC prognosing breast disease. Gene expression analysis is useful for
 CC assessing the toxicity of chemical agents on cells. The microarray of
 CC this invention presents a far greater diversity of probes for measuring
 CC gene expression, with far less bias than expressed sequence tag
 CC microarrays. The method is suitable for rapid production of functional
 CC information from genomic sequence. The present sequence is a peptide
 CC encoded by a single exon nucleic acid probe of the invention. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 41 AA;
 Query Match 100.0%; Score 62; DB 4; Length 41;
 Best Local Similarity 100.0%; Pred. No. 0.00067;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KKKQYTSIHG 11
 |||||
 Db 28 KKKQYTSIHG 38
 RESULT 10
 ABB21071
 ID ABB21071 standard; protein; 41 AA.
 XX AC ABB21071;
 XX DT 23-JAN-2002 (first entry)
 XX DE Protein #3070 encoded by probe for measuring heart cell gene expression.
 XX KW Human; gene expression; heart; microarray; vascular system;
 KW cardiovascular disease; hypertension; cardiac arrhythmia;

KW congenital heart disease.
 XX Homo sapiens.
 XX WO200157274-A2.
 PD 09-AUG-2001.
 XX 30-JAN-2001; 2001WO-US000666.
 XX 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 XX Penn SG, Hanzel DK, Chen W, Rank DR;
 XX WPI; 2001-488899/53.
 XX Single exon nucleic acid probes for analyzing gene expression in human
 PT hearts.
 XX Claim 15; SEQ ID NO 22841; 530pp; English.
 XX The present invention relates to single exon nucleic acid probes for
 CC measuring human gene expression in a sample derived from human heart (see
 CC ABA21535-ABA41305). The present sequence is a protein encoded by one such
 CC probe. The probes may be used for predicting, measuring and displaying
 CC gene expression in samples derived from the human heart via microarrays.
 CC By measuring gene expression, the probes are useful for predicting,
 CC diagnosing, grading, staging, monitoring and prognosing diseases of the
 CC human heart and vascular system e.g. cardiovascular disease, of the
 CC hypertension, cardiac arrhythmias and congenital heart disease. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 41 AA;
 Query Match 100.0%; Score 62; DB 4; Length 41;
 Best Local Similarity 100.0%; Pred. No. 0.00067;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KKKQYTSIHG 11
 |||||
 Db 28 KKKQYTSIHG 38
 RESULT 11
 AAM56438
 ID AAM56438 standard; protein; 41 AA.
 XX

AC AAM56459;
 XX 05-NOV-2001 (first entry)
 DT
 DE Human brain expressed single exon probe encoded protein SEQ ID NO: 28563.
 XX
 XX Human; brain expressed exon; gene expression analysis; probe; microarray;
 KW Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.
 XX
 OS Homo sapiens.
 XX
 PN WO200157275-A2.
 PD
 PD 09-AUG-2001.
 XX
 PF 30-JAN-2001; 2001WO-US000667.
 XX
 PR 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 XX Penn SG, Hanzel DK, Chen W, Rank DR;
 XX
 XX WPI; 2001-483446/52.
 DR
 XX Single exon nucleic acid probes for analyzing gene expression in human
 PT brains.
 PS Example 4; SEQ ID NO 28563; 650pp + Sequence Listing; English.
 XX
 XX The present invention provides a number of single exon nucleic acid
 CC probes which are derived from genomic sequences expressed in the human
 CC brain. They can be used to measure gene expression in brain cell samples,
 CC which may enable the diagnosis and improved treatment of nervous system
 CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
 CC epilepsy and cancers. The present sequence is a protein encoded by one of
 CC the probes of the invention
 XX
 XX Sequence 41 AA;
 SQ
 Query Match 100.0%; Score 62; DB 4; Length 41;
 Best Local Similarity 100.0%; Pred. No. 0.00067;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 KKQVTSIHG 11
 |||||
 Db 28 KKQVTSIHG 38
 RESULT 12
 AAM04374

AAM04374 standard; protein; 41 AA.
 XX
 AC AAM04374;
 XX
 DT 09-OCT-2001 (first entry)
 XX
 DE Peptide #3056 encoded by probe for measuring breast gene expression.
 XX
 XX Probe; human; breast disease; breast cancer; development disorder;
 KW inflammatory disease; proliferative breast disease; non-carcinoma tumour.
 XX
 OS Homo sapiens.
 XX
 PN WO200157270-A2.
 PD
 PD 09-AUG-2001.
 XX
 PF 29-JAN-2001; 2001WO-US000661.
 XX
 PR 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 XX Penn SG, Hanzel DK, Chen W, Rank DR;
 XX
 XX WPI; 2001-476286/51.
 DR
 XX Novel single exon nucleic acid probe used to measuring gene expression in
 PT a human breast.
 PS Claim 27; SEQ ID NO 13114; 322pp; English.
 XX
 XX The present invention relates to novel single exon nucleic acid probes
 CC (see AAI00010-AAI10067). The present sequence is a peptide encoded by one
 CC such probe. The probes are useful for measuring human gene expression in
 CC a human breast sample, where the probe hybridizes at high stringency to a
 CC nucleic acid expressed in the human breast. The probes are useful for
 CC predicting, diagnosing, grading, staging, monitoring and prognosing
 CC diseases of the human breast, particularly those diseases with polygenic
 CC aetiology. The diseases include: breast cancer, disorders of development,
 CC inflammatory diseases of the breast, fibrocystic changes, proliferative,
 CC breast disease and non-carcinoma tumours. Note: The sequence data for
 CC this patent did not form part of the printed specification, but was
 CC obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 41 AA;
 SQ
 Query Match 100.0%; Score 62; DB 4; Length 41;
 Best Local Similarity 100.0%; Pred. No. 0.00067;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKKQYTSIHG 11
 Db 28 KKKQYTSIHG 38

RESULT 13
 ABG38416
 ID ABG38416 standard; peptide; 41 AA.
 AC ABG38416;
 DT 19-AUG-2002 (first entry)
 XX Human peptide encoded by genome-derived single exon probe SEQ ID 28081.
 XX Human; single exon probe; asthma; lung cancer; COPD; ILD;
 KW chronic obstructive pulmonary disease; interstitial lung disease;
 KW familial idiopathic pulmonary fibrosis; neurofibromatosis;
 KW tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
 KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemorrhage;
 KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karagener syndrome;
 KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
 KW primary ciliary dyskinesia; pulmonary hypertension;
 KW hyaline membrane disease.
 XX Homo sapiens.
 OS
 PN WO200186003-A2.
 XX
 XX 15-NOV-2001.
 XX
 XX 30-JAN-2001; 2001WO-US000665.
 XX 04-FEB-2000; 2000US-0180312P.
 XX 26-MAY-2000; 2000US-0207456P.
 XX 30-JUN-2000; 2000US-00609408.
 XX 03-AUG-2000; 2000US-00632366.
 XX 21-SEP-2000; 2000US-0234687P.
 XX 27-SEP-2000; 2000US-0236359P.
 XX 04-OCT-2000; 2000GB-00024263.
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 XX Penn SG, Hanzel DK, Chen W, Rank DR;
 PI WPI; 2002-114183/15.
 XX Spatially-addressable set of single exon nucleic acid probes, used to
 PT measure gene expression in human lung samples.
 XX Claim 27; SEQ ID NO 28081; 634bp; English.
 XX The invention relates to a spatially-addressable set of single exon
 CC nucleic acid probes for measuring gene expression in a sample derived
 CC from human lung comprising single exon nucleic acid probes having one of
 CC 12614 nucleic acid sequences mentioned in the specification, or their

complements or the 12387 open reading frames derived from the 12614
 probes. Also included are a microarray comprising the novel set of probes
 ; the novel set of probes which hybridize at high stringency to a nucleic
 acid expressed in the human lung; measuring gene expression in a sample
 derived from human lung, comprising (a) contacting the array with a
 collection of detectably labeled nucleic acids derived from human lung
 mRNA, and (b) measuring the label detectably bound to each probe of the
 array; identifying exons in a eukaryotic genome, comprising (a)
 algorithmically predicting at least one exon from genomic sequences of
 the eukaryote; and (b) detecting specific hybridization of detectably
 labeled nucleic acids from eukaryotic lung mRNA, to a single exon probe,
 having a fragment identical to the predicted exon, the probe is included
 in the above mentioned microarray; assigning exons to a single gene,
 comprising (a) identifying the expression of each of the exons in several
 tissues and/or cell types using hybridization to a single exon
 microarrays having a probe with the exon, where a common pattern of
 expression of the exons in the tissues and/or cell types indicates that
 the exons should be assigned to a single gene; a peptide comprising one
 of 12011 sequences, mentioned in the specification, or encoded by the
 probes/open reading frames (ORF). The probes are used for gene expression
 analysis, and for identifying exons in a gene, particularly using human
 lung derived mRNA and for the study of lung diseases such as asthma, lung
 cancer, chronic obstructive pulmonary disease (COPD), interstitial lung
 disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,
 CC tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-
 CC Pudiak syndrome, sarcoidosis, pulmonary haemorrhage, pulmonary
 CC histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis,
 CC Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary
 CC dyskinesia, pulmonary hypertension and hyaline membrane disease. The
 CC present sequence is a peptide/protein encoded by a single exon probe of
 the invention. Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic format
 CC directly from WIFO at ftp.wipo.int/pub/published_pat_sequences

XX Sequence 41 AA;
 QY 1 KKKQYTSIHG 11
 Db 28 KKKQYTSIHG 38

Query Match 100.0%; Score 62; DB 5; Length 41;
 Best Local Similarity 100.0%; Pred. No. 0.00067;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 14
 AAW53985
 ID AAW53985 standard; protein; 44 AA.
 XX
 AC AAW53985;
 XX 18-AUG-1998 (first entry)
 XX Human ALZASp2.
 DE
 XX Deas; DSASp; alzas; Down's syndrome; diagnosis; therapy; human;

KW Alzheimer's disease.
 OS Homo sapiens.
 XX
 PN W09807850-A2.
 XX
 PD 26-FEB-1998.
 XX
 XX
 PF 22-AUG-1997; 97WO-EP004599.
 XX
 XX 22-AUG-1996; 96CA-02183901.
 PR
 PA (BERG/) BERGMANN J E.
 PA (PRED/) PREDDIE E R.
 XX
 XX
 PI Bergmann JE, Freddie ER;
 XX
 XX WPI; 1998-169155/15.
 DR N-PSDB; AAV23755.
 XX
 XX Nucleic acid molecules dsas, and alzas - used for detecting and treating
 PT Down's syndrome and Alzheimer's disease.
 XX
 XX Claim 13; Fig 1M; 96pp; English.
 XX
 CC This sequence is the ALZASp2 encoded by the nucleic acid alzas. The dsas
 CC and alzas DNA sequences are the nucleic acids of the invention. Reagents
 CC specifically for DSASP can be used for the diagnosis of Down's syndrome
 CC in humans and especially in pregnant women. Molecules that inhibit the
 CC activity of the promoters (PDS1, PDS2, PDS3, and PDS4) for dsas can be
 CC used for treating Down's syndrome. The reagent capable of detecting alzas
 CC can be used for detecting Alzheimer's disease, especially in the pre-
 CC symptomatic stage. Substances that inhibit the promoters for alzas can be
 CC used in treating Alzheimer's disease
 XX
 XX Sequence 44 AA;
 SQ
 Query Match 100.0%; Score 62; DB 2; Length 44;
 Best Local Similarity 100.0%; Pred. No. 0.00072; Indels 0; Gaps 0;
 Matches 11; Conservative 0; Mismatches 0;
 Qy 1 KKKQYTSIHGG 11
 |||||
 Db 19 KKKQYTSIHGG 29
 |||||
 RESULT 15
 ID AAR58917 standard; peptide; 47 AA.
 XX
 XX AAR58917;
 AC
 XX
 XX 25-VAR-2003 (revised)
 DT 15-APR-1995 (first entry)
 XX
 XX Cytoplasmic tail portion of APP695 (residues 649-695).
 DE
 XX

KW Amyloid precursor protein; APP695; beta amyloid; cytoplasmic tail;
 Alzheimer's disease.
 XX
 OS Homo sapiens.
 XX
 PN W09419692-A1.
 XX
 PD 01-SEP-1994.
 XX
 XX 17-FEB-1994; 94WO-US001712.
 PF
 XX 18-FEB-1993; 93US-00019208.
 PR
 XX (GEO) GEN HOSPITAL CORP.
 PA
 XX
 PI Nishimoto I;
 XX
 XX WPI; 1994-294486/36.
 DR
 XX Identifying cpds. useful for treating or preventing Alzheimer's disease -
 PT by determining whether it interferes with the association of the coupleone
 PT portion of amyloid precursor protein to G polypeptide.
 XX
 XX Claim 4; Page 29; 71pp; English.
 XX
 CC Beta amyloid is synthesized as part of a larger protein referred to as
 CC amyloid precursor protein (APP), which has a number of isoforms in
 CC humans, including APP695 and APP770. The amino terminal of beta amyloid
 CC is generated by cleavage of a peptide bond of APP which in APP695 lies
 CC between Met596 and Asp597. APP forms a complex with Go, a GTP-binding
 CC protein (or "G protein") in brain. Go is made of one alpha subunit and
 CC one Beta-gamma subunit. Two isoforms of Go, known as Go1 (or GoA) and Go2
 CC (or GoB) have been identified; they have slight AA differences in their
 CC alpha subunits. The cDNA sequence and deduced AA sequence of the alpha
 CC subunits in each of Go1 and Go2 are shown in AAQ69002/R58914 and
 CC AAQ69004/R58924 respectively. The cytoplasmic Asp695 sequence His657-
 CC Lys676 (AAR58913) possesses a specific Go-activating function, and is
 CC necessary for complex formation of this APP with Go. The cytoplasmic tail
 CC portion of APP695 from residues 649-695 and the membrane-spanning
 CC segment from residues 625-648 are given in AAR58917, AAR58918, and
 CC AAR58922 respectively. The sequence of all of APP is given in
 CC AAQ69003/R58923. (Updated on 25-MAR-2003 to correct PN field.)
 XX
 XX Sequence 47 AA;
 SQ
 Query Match 100.0%; Score 62; DB 2; Length 47;
 Best Local Similarity 100.0%; Pred. No. 0.00078;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 KKKQYTSIHGG 11
 |||||
 Db 1 KKKQYTSIHGG 11
 |||||
 Search completed: October 4, 2004, 18:52:37
 Job time : 64.8478 secs

OM protein - protein search, using sw model

Run on: October 4, 2004, 18:45:55 ; Search time 16.2609 Seconds
(without alignments)
65.071 Million cell updates/sec

Title: US-10-048-209-4

Perfect score: 62

Sequence: 1 KKQYTSIHGG 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR78:*

1: PIR1:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	62	100.0	82	2 P00438	Alzheimer's disease
2	62	100.0	695	1 A49795	Alzheimer's disease
3	62	100.0	695	2 A27485	Alzheimer's disease
4	62	100.0	695	2 S00550	Alzheimer's disease
5	62	100.0	770	1 QRRUA4	Alzheimer's disease
6	59	95.2	747	2 JHC773	Alzheimer's disease
7	43	69.4	406	2 S76307	hypothetical prote
8	40	64.5	452	2 T04781	hypothetical prote
9	39	62.9	452	2 S58994	NADH2 dehydrogenas
10	38	61.3	488	2 S64140	hypothetical prote
11	37	59.7	142	2 T10871	y4kQ protein - Rhi
12	37	59.7	191	2 A35961	sperm membrane pro
13	37	59.7	267	2 T12381	zinc finger protei

14	37	59.7	391	2 H96517	protein T226.22 [1
15	37	59.7	442	2 A11661	ATP-dependent RNA
16	37	59.7	511	2 JCL404	CDEI-box DNA-bindi
17	37	59.7	653	2 A46362	amyloid precursor-
18	37	59.7	751	2 A49974	beta-amyloid precu
19	37	59.7	763	2 A49321	amyloid beta (A4)
20	37	59.7	765	2 S42880	amyloid precursor-
21	37	59.7	2584	2 T24158	hypothetical prote
22	37	59.7	2606	2 T24157	hypothetical prote
23	36	58.1	119	2 A63136	hypothetical prote
24	36	58.1	273	2 C75529	competence protein
25	36	58.1	412	2 T24023	hypothetical prote
26	36	58.1	443	2 T46532	probable dTDP-4-ke
27	36	58.1	693	2 T49296	hypothetical prote
28	36	58.1	749	2 B69941	ATP-dependent RNA
29	36	58.1	1268	2 B88209	protein K02A2.6 [1
30	36	58.1	1313	2 T29193	hypothetical prote
31	36	58.1	3973	2 B71612	hypothetical prote
32	35	56.5	102	2 T07078	cold stress protei
33	35	56.5	150	2 F96924	flavodoxin import
34	35	56.5	177	2 F94245	inosine-5'-monopho
35	35	56.5	211	2 T01627	probable ATP bindi
36	35	56.5	239	2 T01463	hypothetical prote
37	35	56.5	264	2 T15289	hypothetical prote
38	35	56.5	266	2 I49114	Ly49H - mouse
39	35	56.5	269	2 T16910	hypothetical prote
40	35	56.5	332	2 T25779	hypothetical prote
41	35	56.5	361	2 D83798	phosphoserine amin
42	35	56.5	410	2 A11660	aminopeptidases ho
43	35	56.5	410	2 A01288	aminopeptidases ho
44	35	56.5	412	2 T23385	hypothetical prote
45	35	56.5	443	2 B39794	transcription fact

ALIGNMENTS

RESULT 1

P00438

Alzheimer's disease amyloid A4 protein precursor - rabbit (fragment)

C/Species: Oryctolagus cuniculus (domestic rabbit)

C/Date: 30-Sep-1993 #sequence_revision 19-Oct-1995 #text_change 19-Oct-1995

C/Accession: P00438; C60045

R/Davidson, J.S.; West, R.L.; Kotikalepudi, P.; Maroun, L.E.

A/Title: Sequence and methylation in the beta/A4 region of the rabbit amyloid

precursor protein gene

A/Reference number: P00438; MUID:93075180; PMID:1445331

A/Accession: P00438

A/Molecule type: DNA

A/Residues: 1-82 <DAV>

A/Cross-references: GB:M83558; GB:M83657

R/Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

Brain Res. Mol. Brain Res. 10, 299-305, 1991

A/Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide

in dog, polar bear and five other mammals by cross-species polymerase chain

reaction analysis.

A:Reference number: A60045; MUID:92017079; PMID:1656157
A:Accession: C60045
A:Molecule type: mRNA
A:Residues: 12-68 <OH>
A:Cross-references: EMBL:X56129
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type
C:Proteinase inhibitor homology
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; Down's syndrome

Query Match 100.0%; Score 62; DB 2; Length 82;
Best Local Similarity 100.0%; Pred. No. 0.0002;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKQYTSIHG 11
| | | | | | | | | |
Db 69 KKQYTSIHG 79

RESULT 2
A49795
Alzheimer's disease amyloid beta protein precursor - crab-eating macaque
C:Species: Macaca fascicularis (crab-eating macaque)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A49795
R:Podlasky, M.B.; Tolan, D.R.; Selkoe, D.J.
Am. J. Pathol. 138, 1423-1435, 1991
A:Title: Homology of the amyloid beta protein precursor in monkey and human supports a primate model for beta amyloidosis in Alzheimer's disease.
A:Reference number: A49795; MUID:91273117; PMID:1905108
A:Accession: A49795
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-695 <POD>
A:Cross-references: GB:X58727; NID:9342062; PIDN:AAA36829.1; PID:c342063
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type
C:Proteinase inhibitor homology
C:Keywords: alternative splicing

Query Match 100.0%; Score 62; DB 1; Length 695;
Best Local Similarity 100.0%; Pred. No. 0.0019;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKQYTSIHG 11
| | | | | | | | | |
Db 649 KKQYTSIHG 659

RESULT 3
A27485
Alzheimer's disease amyloid beta/A4 protein homolog precursor - mouse
N:Alternate names: proteinase nexin II
C:Species: Mus musculus (house mouse)
C:Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 13-Aug-1999
C:Accession: A27485; S19727; I49485
R:Yamada, T.; Sasaki, H.; Tsuruya, H.; Miyata, T.; Goto, I.; Sasaki, Y.
Biochem. Biophys. Res. Commun. 149, 665-671, 1987

A:Title: Complementary DNA for the mouse homolog of the human amyloid beta protein precursor.
A:Reference number: A27485; MUID:88106489; PMID:3322280
A:Accession: A27485
A:Molecule type: mRNA
A:Residues: 1-695 <YAM>
A:Cross-references: GB:M18373; NID:9191568; PIDN:AAA37139.1; PID:g309085
R:Experimental source: brain
R:De Strooper, B.; van Leuven, F.; van den Berghe, H.
Biochim. Biophys. Acta 1129, 141-143, 1991
A:Title: The amyloid beta protein precursor or proteinase nexin II from mouse is closer related to its human homolog than previously reported.
A:Reference number: S19727; MUID:92096456; PMID:1756177
A:Accession: S19727
A:Molecule type: mRNA
A:Residues: 1-210, 'G', '212-220, 'S', '222-396, 'A', '398-402, 'T', '404-448, 'A', '450-695 <STR>
A:Cross-references: EMBL:X59379
R:Izumi, R.; Yamada, T.; Yoshikai, S.; Sasaki, H.; Hattori, M.; Sasaki, Y.
Gene 112, 189-195, 1992
A:Title: Positive and negative regulatory elements for the expression of the Alzheimer's disease amyloid precursor-encoding gene in mouse.
A:Reference number: I49485; MUID:92209998; PMID:1555768
A:Accession: I49485
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-19 <RES>
A:Cross-references: GB:D10603; NID:9220328; PIDN:BAA01456.1; PID:g220329
C:Genetics:
A:Map position: 16C3
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type
C:Proteinase inhibitor homology
C:Keywords: alternative splicing; amyloid; transmembrane protein

Query Match 100.0%; Score 62; DB 2; Length 695;
Best Local Similarity 100.0%; Pred. No. 0.0019;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKQYTSIHG 11
| | | | | | | | | |
Db 649 KKQYTSIHG 659

RESULT 4
S00550
Alzheimer's disease amyloid beta protein precursor - rat
N:Alternate names: beta-A4 amyloid protein
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 13-Aug-1999
C:Accession: S00550; A41245; A39820; S46251
R:Shivers, B.D.; Hilbich, C.; Multhaup, G.; Salbaum, M.; Beyreuther, K.; Seeburg, P.H.
EMBO J. 7, 1365-1370, 1988
A:Title: Alzheimer's disease amyloidogenic glycoprotein: expression pattern in rat brain suggests a role in cell contact.
A:Reference number: S00550; MUID:88312583; PMID:2900758
A:Accession: S00550

A/Molecule type: mRNA
A:Residues: 1-695 <SHI>
A:Cross-references: EMBL:X07648; NID:g55616; PID:CAA30488.1; PID:g55617
R:Schubert, D.; Schroeder, R.; LaCorbiere, M.; Saitoh, T.; Cole, G.
Science 241, 223-226, 1988
A>Title: Amyloid beta protein precursor is possibly a heparan sulfate
proteoglycan core protein.
A:Reference number: A41245; MUID:B8264430; PMID:2968652
A:Accession: A41245
A/Molecule type: protein
A:Residues: 18-37, 'X', 39-40, 'X', 42-44 <SCH>
A:Note: evidence for heparan sulfate attachment
R:Hesse, L.; Behr, D.; Masters, C.L.; Multhaup, G.
FEBS Lett. 349, 109-116, 1994
A>Title: The beta-A4 amyloid precursor protein binding to copper.
A:Reference number: S46251; MUID:94320627; PMID:7913895
A:Contents: annotation; copper binding sites
A:Note: rat peptides were isolated but not sequenced
R:Petropaska, A.; Styles, J.; Mehta, P.; Kim, K.S.; Miller, D.L.
J. Biol. Chem. 266, 8464-8469, 1991
A>Title: Purification and tissue level of the beta-amyloid peptide precursor of
rat brain.
A:Reference number: A39820; MUID:91217087; PMID:1673681
A:Accession: A39820
A>Status: preliminary
A/Molecule type: protein
A:Residues: 18-32 <POT>
A:Experimental source: brain
C:Comment: Deposition of amyloid protein as neurofibrillary tangles and/or
plaques is characteristic of both Alzheimer's disease and Down's syndrome.
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type
proteinase inhibitor homology
C:Keywords: alternative splicing; amyloid; glycoprotein; transmembrane protein
F:625-648/Domain: transmembrane #status predicted <TM>

Query Match 100.0%; Score 62; DB 2; Length 695;
Best Local Similarity 100.0%; Pred. No. 0.0019;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKQYTSIHG 11
|||||
Db 649 KKQYTSIHG 659

RESULT 5
QRHUA4
N:Alzheimer's disease amyloid beta protein precursor [validated] - human
N:Alternate names: Alzheimer's disease amyloid A4 protein; coagulation factor
Xia inhibitor; proteinase nexin II (PN-II)
N:Contains: amyloid beta protein long, plaque form; amyloid beta protein short,
vascular form; amyloid protein precursor splice form APP(695); amyloid protein
precursor splice form APP(751); amyloid protein precursor splice form APP(770)
C:Species: Homo sapiens (man)
C>Date: 30-Jun-1987 #sequence revision 28-Jul-1995 #text change 15-Sep-2000
C:Accession: S02260; S05194; A32277; A33260; A35486; I39452; I39451; I39453;
I59562; A44017; B44017; A03134; A25030; A47584; S02638; S00707; S00925;
A38949; A30320; B30320; C30320; A31087; A24668; A28583; A29302; A60605; UJ0036;
S06121; A60355; A59011; A38384; S29076; S38252; S32539; S48148; S48692; S51186;
S51185; S51184; S51183; A54238; I58075; I52250; S09010; S10737; S24127; S43644
R:Lemaire, H.G.; Salbaum, J.M.; Multhaup, G.; Kang, J.; Bayney, R.M.; Unterbeck,
A.; Beyreuther, K.; Mueller-Hill, B.
Nucleic Acids Res. 17, 517-522, 1989
A>Title: The PexA(695) precursor protein of Alzheimer's disease A4 amyloid is
encoded by 16 exons.
A:Reference number: S02260; MUID:89128427; PMID:2783775
A:Accession: S02260
A/Molecule type: DNA
A:Residues: 1-288, 'V', 365-770 <LEM1>
A:Cross-references: EMBL:X13466
A:Note: alternative splice form APP(695)
R:Lemaire, H.G.
submitted to the EMBL Data Library, November 1988
A:Reference number: S05194
A:Accession: S05194
A/Molecule type: DNA
A:Residues: 1-14, 'VM', 17-288, 'V', 365-770 <LEM2>
A:Cross-references: EMBL:X13466; NID:g35998; PID:CAA31830.1; PID:g871360
A:Note: alternative splice form APP(695)
R:la Fauti, G.; Lahiri, D.K.; Salton, S.R.J.; Robakis, N.K.
Biochem. Biophys. Res. Commun. 159, 297-304, 1989
A>Title: Characterization of the 5'-end region and the first two exons of the
beta-protein precursor gene.
A:Reference number: A32277; MUID:89165870; PMID:2538123
A:Accession: A32277
A/Molecule type: DNA
A:Residues: 1-75 <LAF>
A:Cross-references: GB:M24546; GB:M24547; NID:g341202; PID:AAIC3654.1;
PID:g516074
R:Johnstone, E.M.; Chaney, M.O.; Moore, R.E.; Ward, K.E.; Norris, F.H.; Little,
S.P.
Biochem. Biophys. Res. Commun. 163, 1248-1255, 1989
A>Title: Alzheimer's disease amyloid peptide is encoded by two exons and shows
similarity to soybean trypsin inhibitor.
A:Reference number: A33260; MUID:89392030; PMID:2675837
A:Accession: A33260
A/Molecule type: DNA
A:Residues: 656-737 <JOH>
A:Cross-references: GB:M29270; NID:g178663; PID:AA51768.1; PID:g178665
R:Prelli, F.; Levy, E.; van Duinen, S.G.; Bots, G.T.A.M.; Luyendijk, W.;
Frangione, B.
Biochem. Biophys. Res. Commun. 170, 301-307, 1990
A>Title: Expression of a normal and variant Alzheimer's beta-protein gene in
amyloid of hereditary cerebral hemorrhage, Dutch type: DNA and protein
diagnostic assays.
A:Reference number: A35486; MUID:90321244; PMID:2196878
A:Accession: A35486
A/Molecule type: DNA
A:Residues: 672-710 <PRE1>
A:Note: 693-Gln was found in DNA isolated from HCMWA-D patients
R:Yoshikai, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sasaki, Y.
Gene 87, 257-263, 1990
A>Title: Genomic organization of the human amyloid beta-protein precursor gene.
A:Reference number: I39451; MUID:90236318; PMID:2110105
A:Accession: I39452

A/Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-770 <YQSL>
 A/Cross-references: GB:M33112; NID:g178613; PIDN:AAE59502.1; PID:g178616
 A/Accession: I39451
 A/Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-530, 'QWLMEVPAWEAKVGR' <YQ32>
 A/Cross-references: GB:M34873; NID:g178608; PIDN:AAE59501.1; PID:g178615
 R/Yoshikai, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sakaki, Y.
 Gene 102, 291-292, 1991
 A/Reference number: A59020; MUID:91340168; PMID:1308403
 A/Contents: annotation; erratum
 A/Note: revised physical map for reference I39451
 R/Levy, E.; Carman, M.D.; Fernandez-Madrid, I.J.; Power, M.D.; Lieberburg, I.; van Duinen, S.G.; Bots, G.T.; Luyendijk, W.; Frangione, B.
 Science 248, 1124-1126, 1990
 A/Title: Mutation of the Alzheimer's disease amyloid gene in hereditary cerebral hemorrhage, Dutch type.
 A/Reference number: I39453; MUID:90260663; PMID:2111584
 A/Accession: I39453
 A/Status: translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 656-737 <LEV>
 A/Cross-references: GB:M37896; NID:g178618; PIDN:AAE51727.1; PID:g178620
 A/Note: a mutation with 693-Gln is presented
 R/Murrell, J.; Farlow, M.; Ghatti, B.; Benson, M.D.
 Science 254, 97-99, 1991
 A/Title: A mutation in the amyloid precursor protein associated with hereditary Alzheimer's disease.
 A/Reference number: I59562; MUID:92022553; PMID:1925564
 A/Accession: I59562
 A/Status: translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 689-716, 'F' 718-737 <MUR>
 A/Cross-references: GB:557665; NID:g236720; PIDN:AAE19991.1; PID:g236721
 R/Kamino, K.; Orr, H.T.; Payami, H.; Wilman, E.M.; Alonso, M.E.; Pulst, S.M.; Anderson, L.; O'dahl, S.; Nemens, E.; White, J.A.; Sadvnick, A.D.; Ball, M.J.; Kaye, J.; Warren, A.; McInnis, M.; Antonarakis, S.E.; Korenberg, J.R.; Sharma, V.; Kukull, W.; Larson, E.; Heaton, L.L.; Martin, G.M.; Bird, T.D.; Schellenberg, G.D.
 Am. J. Hum. Genet. 51, 998-1014, 1992
 A/Title: Linkage and mutational analysis of familial Alzheimer disease kindreds for the APP gene region.
 A/Reference number: A44017; MUID:93035397; PMID:1415269
 A/Accession: A44017
 A/Molecule type: DNA
 A/Residues: 687-692, 'G' 694-718 <KAM1>
 A/Cross-references: GB:S45135; NID:g257377; PIDN:AAE23645.1; PID:g257378
 A/Experimental source: familial Alzheimer disease family SB
 A/Note: sequence extracted from NCBI backbone (NCBIP:115374)
 A/Accession: B44017
 A/Molecule type: DNA
 A/Residues: 687-718 <KAM2>
 A/Cross-references: GB:S45136; NID:g257379; PIDN:AAE23646.1; PID:g257380

A/Experimental source: familial Alzheimer disease family LIT
 A/Note: sequence extracted from NCBI backbone (NCBIP:115376)
 R/Kang, J.; Lemaire, H.G.; Unterbeck, A.; Salbaum, J.M.; Masters, C.L.; Grzeschik, K.H.; Multhaup, G.; Beyreuther, K.; Muller-Hill, B.
 Nature 325, 733-736, 1987
 A/Title: The precursor of Alzheimer's disease amyloid A4 protein resembles a cell-surface receptor.
 A/Reference number: A03134; MUID:87144572; PMID:2881207
 A/Accession: A03134
 A/Molecule type: mRNA
 A/Residues: 1-288, 'V' 365-770 <KAN>
 A/Cross-references: GB:Y00264; NID:g28525; PIDN:CAA68374.1; PID:g28526
 A/Note: alternative splice form APP(695)
 R/Kobakis, N.K.; Ramakrishna, N.; Wolfe, G.; Wisniewski, H.M.
 Proc. Natl. Acad. Sci. U.S.A. 84, 4190-4194, 1987
 A/Title: Molecular cloning and characterization of a cDNA encoding the cerebrovascular and the neuritic plaque amyloid peptides.
 A/Reference number: A29030; MUID:87231971; PMID:3035574
 A/Accession: A29030
 A/Molecule type: mRNA
 A/Residues: 284-288, 'V' 365-646, 'E' 648-770 <ROB>
 A/Cross-references: GB:M16765; NID:g178539; PIDN:AAE51722.1; PID:g178540
 A/Note: the authors translated the codon GAG for residue 647 as Asp
 R/Goldgaber, D.; Lerman, M.I.; McBride, O.W.; Saffioti, U.; Gajdusek, D.C.
 Science 235, 877-880, 1987
 A/Title: Characterization and chromosomal localization of a cDNA encoding brain amyloid of Alzheimer's disease.
 A/Reference number: A47584; MUID:87120328; PMID:3810169
 A/Accession: A47584
 A/Molecule type: mRNA
 A/Residues: 674-756, 'S' 758-770 <GOL>
 A/Cross-references: GB:M15533; NID:g178706; PIDN:AAA35540.1; PID:g178707
 A/Experimental source: brain
 R/Tanzi, R.E.; Gusella, J.F.; Watkins, P.C.; Bruns, G.A.P.; St George-Hyslop, P.; Van Keuren, M.L.; Patterson, D.; Fagan, S.; Kurnit, D.M.; Neve, R.L.
 Science 235, 880-884, 1987
 A/Title: Amyloid beta protein gene: cDNA, mRNA distribution, and genetic linkage near the Alzheimer locus.
 A/Reference number: A47585; MUID:87120329; PMID:2949367
 A/Accession: A47585
 A/Molecule type: mRNA
 A/Residues: 674-703 <TANI>
 A/Cross-references: GB:M15532; NID:g177957; PIDN:AAA51564.1; PID:g177958
 R/Dyck, T.; Weidemann, A.; Multhaup, G.; Salbaum, J.M.; Lemaire, H.G.; Kang, J.; Mueller-Hill, B.; Masters, C.L.; Beyreuther, K.
 EMBO J. 7, 949-957, 1988
 A/Title: Identification, transmembrane orientation and biogenesis of the amyloid A4 precursor of Alzheimer's disease.
 A/Reference number: S02638; MUID:88296437; PMID:2900137
 A/Accession: S02638
 A/Molecule type: mRNA
 A/Residues: 672-678 <DYR>
 R/Tanzi, R.E.; McClatchey, A.I.; Lamperti, E.D.; Villa-Komaroff, L.; Gusella, J.F.; Neve, R.L.
 Nature 331, 528-530, 1988

A/Title: Protease inhibitor domain encoded by an amyloid protein precursor mRNA associated with Alzheimer's disease.
A/Reference number: S00707; MUID:88122640; PMID:2893290
A/Accession: S00707
A/Molecule type: mRNA
A/Residues: 286-344, 'I', 365-366 <TAN2>
A/Cross-references: EMBL:X06982; NID:g28817; PIDN:CAA30042.1; PID:g29612
A/Experimental source: promyelocytic leukemia cell line HL60
A/Note: alternative splice form APP(751)
R/Ponte, P.; Gonzalez-Dawhitt, P.; Schilling, J.; Muller, J.; Hsu, D.; Greenberg, B.; Davis, K.; Wallace, W.; Lieberburg, I.; Fuller, F.; Cordell, B.
Nature 331, 525-527, 1988
A/Title: A new A4 amyloid mRNA contains a domain homologous to serine proteinase inhibitors.
A/Reference number: S00925; MUID:88122639; PMID:2893289
A/Accession: S00925
A/Molecule type: mRNA
A/Residues: 1-344, 'I', 365-770 <PO2>
A/Cross-references: GB:X06989; EMBL:X00297; NID:g28720; PIDN:CAA30050.1; PID:g28721
A/Note: alternative splice form APP(751)
R/Kitaguchi, N.; Takahashi, Y.; Tokushima, Y.; Shiojiri, S.; Ito, H.
Nature 331, 530-532, 1988
A/Title: Novel precursor of Alzheimer's disease amyloid protein shows protease inhibitory activity.
A/Reference number: A38949; MUID:88122641; PMID:2893291
A/Accession: A38949
A/Molecule type: mRNA
A/Residues: 287-367 <K17>
A/Cross-references: GB:X06981; NID:g28816; PIDN:CAA30041.1; PID:g292611
A/Experimental source: glioblastoma cell line
A/Note: alternative splice form APP(770)
R/Vitek, M.P.; Rasool, C.G.; de Sauvage, F.; Vitek, S.M.; Bartus, R.T.; Beer, B.; Ashton, R.A.; Macq, A.F.; Maloteaux, J.M.; Blume, A.J.; Octave, J.N.
Brain Res. Mol. Brain Res. 4, 121-131, 1988
A/Title: Absence of mutation in the beta-amyloid cDNAs cloned from the brains of three patients with sporadic Alzheimer's disease.
A/Reference number: A30320
A/Accession: A30320
A/Status: not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 284-286, 'I', 365-770 <VIT1>
A/Accession: B30320
A/Status: not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 122-288, 'I', 365-770 <VIT2>
A/Accession: C30320
A/Status: not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 606-770 <VIT3>
R/Zain, S.B.; Salim, M.; Chou, W.G.; Sajdel-Sulkowska, E.M.; Majocha, R.E.; Marotta, C.A.
Proc. Natl. Acad. Sci. U.S.A. 85, 929-933, 1988
A/Title: Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer disease brain: coding and noncoding regions of the fetal precursor mRNA are expressed in the cortex.
A/Reference number: A31087; MUID:88124954; PMID:2893379

A/Accession: A31087
A/Molecule type: mRNA
A/Residues: 507-770 <ZAI>
A/Cross-references: GB:M18734; NID:g178572; PIDN:AAA51726.1; PID:g178573
A/Note: the authors translated the codon GAA for residue 599 as Gly, ACC for residue 603 as Val, GGG for residue 604 as Glu, GAG for residue 605 as Leu, CTT for residue 607 as Pro, CCC for residue 608 as Val, GIG for residue 609 as Asn, AAT for residue 610 as Gly, and GGT for residue 635 as Ser
A/Note: the cited Genbank accession number, J03594, is not in release 101.0
R/Masters, C.L.; Multhaup, G.; Simms, G.; Pottgiesser, J.; Martins, R.N.; Beyreuther, K.
Query Match 100.0%; Score 62; DB 1; Length 770;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KKKQYTSIHGG 11
IIIIIIIIII
Db 724 KKKQYTSIHGG 734
RESULT 6
JH0773
Alzheimer's disease amyloid beta protein precursor - African clawed frog
C/Species: Xenopus laevis (African clawed frog)
C/Date: 10-Jun-1993 #sequence_revision 10-Jun-1993 #text_change 13-Aug-1999
C/Accession: JH0773
R/Okado, H.; Okamoto, H.
Biochem. Biophys. Res. Commun. 189, 1561-1568, 1992
A/Title: A Xenopus homologue of the human beta-amyloid precursor protein: developmental regulation of its gene expression.
A/Reference number: JH0773; MUID:93129227; PMID:1282805
A/Accession: JH0773
A/Molecule type: mRNA
A/Residues: 1-747 <OKA>
A/Cross-references: GB:S52417; NID:g263150; PIDN:AAB24853.1; PID:g263151
A/Experimental source: larva
C/Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase inhibitor homology
C/Keywords: alternative splicing; amyloid
F:287-337/Domain: animal Kunitz-type proteinase inhibitor homology <BP1>
Query Match 95.2%; Score 59; DB 2; Length 747;
Best Local Similarity 90.9%; Pred. No. 0.0075;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KKKQYTSIHGG 11
IIIIIIIIII
Db 701 KKKQYTSIHGG 711
Search completed: October 4, 2004, 18:58:25
Job time : 18.2609 secs

OM protein - protein search, using sw model

Run on: October 4, 2004, 18:44:39 ; Search time 9.09696 Seconds
(without alignments)
63.032 Million cell updates/sec

Title: US-10-048-209-4

Perfect score: 62

Sequence: 1 KKQGYTSIHG 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.4

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	62	100.0	751	A4_SAIISC	Q95241 s amyloid b
2	62	100.0	770	A4_CAVPO	Q60495 c amyloid b
3	62	100.0	770	A4_HUMAN	P05067 h amyloid b
4	62	100.0	770	A4_NACFA	P53601 m amyloid b
5	62	100.0	770	A4_MOUSE	P12023 m amyloid b
6	62	100.0	770	A4_PIG	P79307 s amyloid b
7	62	100.0	770	A4_RAT	P08592 r amyloid b
8	59	95.2	737	A4_FUGRU	Q93279 flugu rubrip
9	59	95.2	780	A4_TETEL	Q73683 tetraodon.f
10	43	69.4	379	ISP8_SINY3	Q55843 synechocyst
11	39	62.9	452	NUAM_LUMTE	Q44949 lumbricus t
12	38	61.3	488	YGM9_YEAST	Q01163 saccharomyc
13	37	59.7	142	Y4KQ_RHISN	P55535 rhizobium s
14	37	59.7	653	APP1_MOUSE	Q03157 mus musculu
15	37	59.7	659	CYOB_BUCAP	Q8K994 buchnera ap
16	37	59.7	695	APP2_MOUSE	Q06335 mus musculu
17	37	59.7	763	APP2_HUMAN	Q06481 homo sapien

18	37	59.7	765	1	APP2_RAT	P15943 rattus norv
19	36	58.1	693	1	SC13_ARATH	Q9Fq19 arabidopsis
20	36	58.1	749	1	YPR4_BACSU	P50830 bacillus su
21	36	58.1	1268	1	YRD6_CAEEL	Q09575 caenorhabdi
22	35	56.5	177	1	RELX_MESAU	Q64171 mesoricetu
23	35	56.5	197	1	PSD9_CAEEL	Q10920 caenorhabdi
24	35	56.5	211	1	14P_ARATH	Q64628 arabidopsis
25	35	56.5	266	1	KLR8_MOUSE	Q60682 mus musculu
26	35	56.5	361	1	SERC_BACHD	Q9Kdm4 bacillus ha
27	35	56.5	412	1	RBAL_CAEEL	P09171 caenorhabdi
28	35	56.5	443	1	GAT3_HUMAN	P23771 homo sapien
29	35	56.5	443	1	GAT3_MOUSE	P23772 mus musculu
30	35	56.5	497	1	DTPT_LACHE	O07380 lactobacill
31	35	56.5	516	1	Y067_MYCGE	P47313 mycoplasma
32	35	56.5	739	1	PURL_LISIN	Q92an9 listeria in
33	35	56.5	739	1	PURL_LISMO	Q8yeci listeria mo
34	35	56.5	753	1	CAT2_NEOCR	Q8x182 neurospora
35	35	56.5	782	1	MUS2_SRAEP	Q8cpl6 staphylococ
36	34	54.8	207	1	ATIS5_BOVIN	Q9tt92 bos taurus
37	34	54.8	249	1	CREB_CHLVR	P51984 chlorohydra
38	34	54.8	348	1	NTRB_PROVU	P28788 proteus vul
39	34	54.8	366	1	TF3A_XENLA	P03001 xenopus lae
40	34	54.8	402	1	ISPH_ANASP	P36674 anabaena sp
41	34	54.8	580	1	SYD_MYCPE	Q8ew67 mycoplasma
42	34	54.8	650	1	APP1_HUMAN	P18547 porcine par
43	34	54.8	660	1	VNCS_PAVPK	P52502 porcine par
44	34	54.8	662	1	VNCS_PAVPK	P52502 porcine par
45	34	54.8	729	1	KEX1_YEAST	P09620 saccharomyc

ALIGNMENTS

RESULT 1

A4_SAIISC					
ID	A4_SAIISC	STANDARD;	PRT;	751	AA.
AC	Q95241;				
DT	15-DEC-1988	(Rel. 37, Created)			
DT	15-DEC-1988	(Rel. 37, Last sequence update)			
DT	10-OCT-2003	(Rel. 42, Last annotation update)			
DE	Amyloid beta A4 protein precursor (APP) (Alzheimer's disease amyloid				
DE	protein homolog) [Contains: Soluble APP-alpha (S-APP-alpha); Soluble				
DE	APP-beta (S-APP-beta); C99; Beta-amyloid protein 42 (Beta-APP42);				
DE	Beta-amyloid protein 40 (Beta-APP40); C83; P3(42); P3(40); Gamma-				
DE	CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-CTF(57)				
DE	(Gamma-secretase C-terminal fragment 57); Gamma-CTF(50) (Gamma-				
DE	secretase C-terminal fragment 50); C31].				
GN	APP.				
OS	Saimiri sciureus (Common squirrel monkey).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Saimiri.				
OX	NCBI_TaxID=9521;				
	[1]				
RN	SEQUENCE FROM N.A.				
RP	TISSUE=Kidney, and Liver;				
RC	MEDLINE=96105492; PubMed=8532114;				
RX	Levy E., Amorim A., Frangione B., Walker L.C.;				
RA					

RT "Beta-amyloid precursor protein gene in squirrel monkeys with
 RL cerebral amyloid angiopathy.";
 CC Neurobiol. Aging 16:803-808(1995).
 CC
 CC -|- FUNCTION: Functions as a cell surface receptor and performs
 CC physiological functions on the surface of neurons relevant to
 CC neurite growth, neuronal adhesion and axonogenesis. Involved in
 CC cell motility and transcription regulation through protein-protein
 CC interactions (By similarity). Can promote transcription activation
 CC through binding to APBB1/Tip60 and inhibit Notch signaling through
 CC interaction with Numb (By similarity). Couples to apoptosis-
 CC inducing pathways such as those mediated by G(O) and JIP (By
 CC similarity). Inhibits G(O) alpha Aase activity (By similarity).
 CC Acts as a kinase I membrane receptor, mediating the axonal
 CC transport of beta-secretase and presenilin 1 (By similarity). May
 CC be involved in copper homeostasis/oxidative stress through copper
 CC ion reduction. In vitro, copper-metalated APP induces neuronal
 CC death directly or is potentiated through Cu(I)-mediated low-
 CC density lipoprotein oxidation (By similarity). Can regulate
 CC neurite outgrowth through binding to components of the
 CC extracellular matrix such as heparin and collagen I and IV (By
 CC similarity). The splice isoforms that contain the BPTI domain
 CC possess protease inhibitor activity (By similarity).
 CC -|- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
 CC with metal-reducing activity. Bind transient metals such as
 CC copper, zinc and iron (By similarity).
 CC -|- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
 CC peptides, including C31, are potent enhancers of neuronal
 CC apoptosis (By similarity).
 CC -|- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
 CC cytoplasmic proteins, including APBB family members, the APBA
 CC family, MAPKIP1, and SHC1, Numb and Dab1 (By similarity). Binding
 CC to Dab1 inhibits its serine phosphorylation (By similarity). Also
 CC interacts with GPCR-like protein BPP, FPR1L1, APPB21, IBL, KNS2
 CC (via its TPR domains) (By similarity), APPB22 (via BASS) and DD31.
 CC In vitro, it binds MAP1 via the MT-binding domains (By
 CC similarity). Associates with microtubules in the presence of ATP
 CC and in a kinesin-dependent manner (By similarity).
 CC -|- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
 CC protein that rapidly becomes internalized via clathrin-coated
 CC pits. During maturation, the immature APP (N-glycosylated in the
 CC endoplasmic reticulum) moves to the Golgi complex where complete
 CC maturation occurs (O-glycosylated and sulfated). After alpha-
 CC secretase cleavage, soluble APP is released into the extracellular
 CC space and the C-terminal is internalized to endosomes and
 CC lysosomes. Some APP accumulates in secretory transport vesicles
 CC leaving the late Golgi compartment and returns to the cell
 CC surface. Gamma-CTF(59) peptide is located to both the cytoplasm
 CC and nuclei of neurons (By similarity).
 CC -|- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms=2;
 CC . Comment=Additional isoforms seem to exist;
 CC Name=APP770;
 CC IsoId=Q95241-1; Sequence=Displayed;
 CC Name=APP695;
 CC IsoId=Q95241-2; Sequence=Not described;
 CC -|- DOMAIN: The basolateral sorting signal (BASS) is required for
 CC sorting of membrane proteins to the basolateral surface of
 CC epithelial cells (By similarity).
 CC -|- DOMAIN: The NPXY sequence motif found in many tyrosine-
 CC phosphorylated proteins is required for the specific binding of
 CC the PID domain. However additional amino acids either N- or C-
 CC terminal to the NPXY motif are often required for complete
 CC interaction. The PID domain-containing proteins which bind APP
 CC require the YENPTY motif for full interaction. These interactions
 CC are independent of phosphorylation on the terminal tyrosine
 CC residue. The NPXY site is also involved in clathrin-mediated
 CC endocytosis (By similarity).
 CC -|- PTM: Proteolytically processed under normal cellular conditions.
 CC Cleavage by alpha-secretase or alternatively by beta-secretase
 CC leads to generation and extracellular release of soluble APP
 CC peptides, S-APP-alpha and S-APP-beta, respectively, and the
 CC retention of corresponding membrane-anchored C-terminal fragments,
 CC C83 and C99. Subsequent processing of C83 by gamma-secretase
 CC yields P3 peptides. This is the major secretory pathway and is
 CC nonamyloidogenic. Alternatively, presenilin/nicastrin-mediated
 CC gamma-secretase processing of C99 releases the amyloid beta
 CC proteins, amyloid-beta 40 (Abeta40) and amyloid-beta 42 (Abeta42),
 CC major components of amyloid plaques, and the cytotoxic C-terminal
 CC fragments, gamma-CTF(50), gamma-CTF(57) and gamma-CTF(59) (By
 CC similarity).
 CC -|- PTM: Proteolytically cleaved by caspases during neuronal apoptosis
 CC (By similarity). Cleavage at Asp-720 by either caspase-3, -8 or -9
 CC results in the production of the neurotoxic C31 peptide and the
 CC increased production of beta-amyloid peptides (By similarity).
 CC -|- PTM: N- and O-glycosylated (By similarity).
 CC -|- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and
 CC serine residues is neuron-specific. Phosphorylation can affect APP
 CC processing, neuronal differentiation and interaction with other
 CC proteins (By similarity).
 CC -|- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and
 CC zinc, can induce histidine-bridging between beta-amyloid molecules
 CC resulting in beta-amyloid-metal aggregates (By similarity).
 CC Extracellular zinc-binding increases binding of heparin to APP and
 CC inhibits collagen-binding (By similarity).
 CC -|- SIMILARITY: Belongs to the APP family.
 CC -|- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC DR EVBL; S81024; AADI4347.1; -;
 CC DR HSP; P03067; IAMP.
 CC DR InterPro; IPR008155; A4_APP.
 CC DR InterPro; IPR008154; A4_extra.
 CC DR InterPro; IPR001255; Beta-APP.
 CC DR InterPro; IPR002223; Kunitz_BPTI.
 CC DR Pfam; PF02177; A4_EXTRA; 1.
 CC DR Pfam; PF03494; Beta-APP; 1.
 CC DR Pfam; PF00014; Kunitz_BPTI; 1.

DR PRINTS; PRO0203; ANKLOIDA4.
DR PRINTS; PRO0739; BASICPHASE.
DR ProDom; PD00022; Kunitz_BPTI; 1.
DR SMART; SMO006; A4_EXTRA; 1.
DR SMART; SMO0131; KU; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
KW Apoptosis; Endocytosis; Cell adhesion; Serine protease inhibitor;
KW Coated pit; Neurone; Heparin-binding; Metal-binding; Copper; Iron;
KW Zinc; Signal; Transmembrane; Glycoprotein; Phosphorylation;
KW Proteoglycan; Amyloid; Alternative splicing.
FT SIGNAL 1 17
FT CHAIN 18 751
FT CHAIN 18 668
FT CHAIN 18 652
FT CHAIN 653 751
FT CHAIN 653 694
FT CHAIN 653 692
FT CHAIN 669 751
FT CHAIN 669 692
FT CHAIN 693 751
FT CHAIN 693 692
FT CHAIN 702 751
FT CHAIN 702 692
FT CHAIN 721 751
FT CHAIN 721 680
FT TRANSMEM 681 704
FT DOMAIN 705 751
FT DOMAIN 96 110
FT DOMAIN 181 188
FT DOMAIN 291 341
FT DOMAIN 316 344
FT DOMAIN 363 428
FT DOMAIN 504 521
FT DOMAIN 713 732
FT DOMAIN 230 260
FT DOMAIN 274 280
FT SITE 144 144
FT ACT_SITE 301 302
FT SITE 652 653
FT SITE 653 654
FT SITE 666 669
FT SITE 685 685
FT SITE 687 687
FT SITE 692 693
FT SITE 694 695
FT SITE 701 702

FT SITE 705 715 (BY SIMILARITY).
FT SITE 720 721 BASOLATERAL SORTING SIGNAL
FT SITE 738 741 (BY SIMILARITY).
FT SITE 740 743 CLEAVAGE (BY CASPASE-3,-6,-8 OR -9)
FT SITE 743 741 (BY SIMILARITY).
FT SITE 740 743 ENDOCYTOSIS SIGNAL.
FT SITE 743 741 NPKY MOTIF.
Query Match 100.0%; Score 62; DB 1; Length 751;
Best Local Similarity 100.0%; Fred. No. 0.0006;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KKQYTSIHGG 11
Db 705 KKQYTSIHGG 715
RESULT 2
A4_CAVPO STANDARD; PRT; 770 AA.
ID A4_CAVPO
AC Q60495; Q60496;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Amyloid beta A4 protein precursor (APP) (ASPP) (Alzheimer's disease
DE amyloid protein homolog) [Contains: Soluble APP-alpha (S-APP-alpha);
DE Soluble APP-beta (S-APP-beta); CTF-alpha; CTF-beta; Beta-amyloid
DE protein 42 (Beta-APP42); Beta-amyloid protein 40 (Beta-APP40); P3(42);
DE P3(40); CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-
DE CTF(57) (Gamma-secretase C-terminal fragment 57); C31].
GN APP.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RC TISSUE=Brain, and Liver;
RX MEDLINE=97236426; PubMed=9116031;
RA Beck M., Mueller D., Bigl V.;
RT "Amyloid precursor protein in Guinea pigs - complete cDNA sequence and
RT alternative splicing."
RL Biochim. Biophys. Acta 1351:17-21(1997).
RN [2]
RP INTERACTION OF BETA-APP40 WITH APOE.
RX MEDLINE=98007700; PubMed=9349344;
RA Martel C.B., Mackic J.B., Matsubara E., Governale S., Miguel C.,
RA Miao W., McComb J.G., Frangione B., Ghiso J., Zlokovic B.V.;
RT "Isoform-specific effects of apolipoproteins E2, E3, and E4 on
RT cerebral capillary sequestration and blood-brain barrier transport of
RT circulating Alzheimer's amyloid beta."
RL J. Neurochem. 69:1995-2004(1997).
RN [3]
RP PROCESSING.
RX MEDLINE=20084499; PubMed=10619481;
RA Beck M., Brueckner M.K., Holzer M., Keep S., Pannicke T., Arendt T.,
RA Bigl V.;

RT "Guinea-pig primary cell cultures provide a model to study expression
RT and amyloidogenic processing of endogenous amyloid precursor
RT protein.";
RL Neuroscience 95:243-254(2000).
RN [4]
RX GAMMA-SECRETASE PROCESSING.
RA MEDLINE:20576391; PubMed:11035007;
RA Pinnix I., Musunuru U., Tun H., Sridharan A., Golde T., Eckman C.,
RA Ziani-Cherif C., Onstead L., Sambamurti K.;
RT "A novel gamma-secretase assay based on detection of the putative
RT C-terminal fragment-gamma of amyloid beta protein precursor.";
RL J. Biol. Chem. 276:481-487(2001).
CC -|- FUNCTION: Functions as a cell surface receptor and performs
CC physiological functions on the surface of neurons relevant to
CC neurite growth, neuronal adhesion and axonogenesis. Involved in
CC cell motility and transcription regulation through protein-protein
CC interactions (By similarity). Can promote transcription activation
CC through binding to APPB1/Tip60 and inhibit Notch signaling through
CC interaction with Numb (By similarity). Couples to apoptosis-
CC inducing pathways such as those mediated by G10 and JIP (By
CC similarity). Inhibits G10 alpha APase activity (By similarity).
CC Acts as a kinesin I membrane receptor, mediating the axonal
CC transport of beta-secretase and presenilin 1 (By similarity). May
CC be involved in copper homeostasis/oxidative stress through copper
CC ion reduction (By similarity). In vitro, copper-metallated APP
CC induces neuronal death directly or is potentiated through Cu(II)-
CC mediated low-density lipoprotein oxidation (By similarity). Can
CC regulate neurite outgrowth through binding to components of the
CC extracellular matrix such as heparin and collagen I and IV (By
CC similarity). The splice isoforms that contain the EPT1 domain
CC possess protease inhibitor activity (By similarity).
CC -|- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
CC with metal-reducing activity. Bind transient metals such as
CC copper, zinc and iron. Beta-amyloid peptides bind to lipoproteins
CC and apolipoproteins E and J in the CSF and to HDL particles in
CC plasma, inhibiting metal-catalyzed oxidation of lipoproteins.
CC -|- FUNCTION: Apicicans elicit adhesion of neural cells to the
CC extracellular matrix and may regulate neurite outgrowth in the
CC brain (By similarity).
CC -|- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
CC peptides, including C31, are potent enhancers of neuronal
CC apoptosis (By similarity).
CC -|- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
CC cytoplasmic proteins, including APBB family members, the APBA
CC family, MAPK81P1, SHC1 and Numb and Dab1 (By similarity). Also
CC interacts with GPCR-like protein BPP, FPR11, APPBP1, IBL, KNS2
CC (via its TPR domains), APPBP2 (via BASS) and DDB1 (By similarity).
CC Associates with microtubules in the presence of ATP and in a
CC kinesin-dependent manner (By similarity). Soluble Abeta40 binds
CC all three isoforms of APOE, in vitro and in vivo. When lipidated,
CC ApoE3 appears to be the preferred amyloid binding isoform, while
CC the apoE4 isoform-beta-APP40 complex is capable of being
CC transported across the blood-brain barrier.
CC -|- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
CC protein that rapidly becomes internalized via clathrin-coated pits
CC (By similarity). During maturation, the immature APP (N-
CC glycosylated in the endoplasmic reticulum) moves to the Golgi

CC complex where complete maturation occurs (O-glycosylated and
CC sulfated) (By similarity). After alpha-secretase cleavage, soluble
CC APP is released into the extracellular space and the C-terminal is
CC internalized to endosomes and lysosomes (By similarity). Some APP
CC accumulates in secretory transport vesicles leaving the late Golgi
CC compartment and returns to the cell surface (By similarity). APP
CC sorts to the basolateral surface in epithelial cells (By
CC similarity).
CC -|- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=2;
CC Comment-Additional isoforms, missing exons 7,8 and 15, seem to
CC exist. The L-isoforms, missing exon 15, are referred to as
CC apicicans;
CC Name=APP770;
CC IsoId=Q60495-1; Sequence=Displayed;
CC Name=APP695;
CC IsoId=Q60495-2; Sequence=VSP_007221, VSP_007222;
CC -|- TISSUE SPECIFICITY: Isoform APP695 is the major isoform found in
CC brain. The longer isoforms containing the EPT1 domain are
CC predominantly expressed in peripheral organs such as muscle and
CC liver.
CC -|- INDUCTION: Increased levels during neuronal differentiation.
CC -|- DOMAIN: The basolateral sorting signal (BASS) is required for
CC sorting of membrane proteins to the basolateral surface of
CC epithelial cells.
CC -|- DOMAIN: The NPXY sequence motif found in many tyrosine-
CC phosphorylated proteins is required for the specific binding of
CC the PID domain. However additional amino acids either N- or C-
CC terminal to the NPXY motif are often required for complete
CC interaction. The PID domain-containing proteins which bind APP
CC require the YENPTY motif for full interaction. These interactions
CC are independent of phosphorylation on the terminal tyrosine
CC residue (By similarity). The NPXY site is also involved in
CC clathrin-mediated endocytosis.
CC -|- PTM: Proteolytically processed under normal cellular conditions.
CC Cleavage by alpha-secretase or alternatively by beta-secretase
CC leads to generation and extracellular release of soluble APP
CC peptides, S-APP-alpha and S-APP-beta, respectively, and the
CC retention of corresponding membrane-anchored C-terminal fragments,
CC CTF-alpha and CTF-beta. Subsequent processing of CTF-alpha by
CC gamma-secretase yields P3 peptides. This is the major secretory
CC pathway and is nonamyloidogenic. Alternatively,
CC presenilin/nicastrin-mediated gamma-secretase processing of CTF-
CC beta releases the amyloid beta proteins, amyloid-beta 40 (Abeta40)
CC and amyloid-beta 42 (Abeta42), major components of amyloid
CC plaques, and the corresponding cytotoxic C-terminal fragments
CC (CTFs).
CC -|- PTM: Proteolytically cleaved by caspase-3 during neuronal
CC apoptosis (By similarity).
CC -|- PTM: N- and O-glycosylated. O-linkage of chondroitin sulfate to
CC the L-APP isoforms produces the APP proteoglycan core proteins,
CC the apicicans (By similarity).
CC -|- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and
CC serine residues is neuron-specific (By similarity).
CC Phosphorylation can affect APP processing, neuronal
CC differentiation and interaction with other proteins.
CC -|- PTM: Extracellular binding and reduction of copper, results in a

CC corresponding oxidation of Cys-144 and Cys-158, and the formation
 CC of a disulfide bond (By similarity).
 CC -|- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and
 CC zinc, can induce histidine-bridging between beta-amyloid molecules
 CC resulting in beta-amyloid-metal aggregates.
 CC -|- SIMILARITY: Belongs to the APP family.
 CC -|- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
 CC
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 CC
 CC EMBL; X97631; CAA65230.1; -;
 CC EMBL; X95198; CAA67589.1; -;
 CC HSSP; P05067; 1BA4.
 CC InterPro; IPR008155; A4_APP.
 CC InterPro; IPR008154; A4_extra.
 CC InterPro; IPR002223; Kunitz_BPTI.
 CC Pfam; PF00014; Kunitz_BPTI; 1.
 CC PRINTS; PR00203; AMYLOIDA4.
 CC PRINTS; PR00759; BASICTPASE.
 CC ProDom; PD000222; Kunitz_BPTI; 1.
 CC SMART; SM00006; A4_EXTRA; 1.
 CC SMART; SM00131; KU; 1.
 CC PROSITE; PS00319; A4_EXTRA; 1.
 CC PROSITE; PS00320; A4_INTRA; 1.
 CC PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 CC PROSITE; PS00279; BPTI_KUNITZ_2; 1.
 CC Apoptosis; Endocytosis; Cell adhesion; Serine protease inhibitor;
 CC Coated pits; Neurone; Hepatin-binding; Metal-binding; Copper; Iron;
 CC Zinc; Signal; Transmembrane; Glycoprotein; Phosphorylation;
 CC Proteoglycan; Alternative splicing; Amyloid.
 CC SIGNAL 1 17 BY SIMILARITY.
 CC CHAIN 18 770 AMYLOID BETA A4 PROTEIN.
 CC CHAIN 18 697 SOLUBLE APP-ALPHA (BY SIMILARITY).
 CC CHAIN 18 671 SOLUBLE APP-BETA (BY SIMILARITY).
 CC CHAIN 672 770 CTF-ALPHA (BY SIMILARITY).
 CC CHAIN 672 713 BETA-AMYLOID PROTEIN 42 (BY SIMILARITY).
 CC CHAIN 672 711 BETA-AMYLOID PROTEIN 40 (BY SIMILARITY).
 CC CHAIN 688 770 CTF-BETA (BY SIMILARITY).
 CC CHAIN 688 713 P3(42) (BY SIMILARITY).
 CC CHAIN 688 711 P3(40) (BY SIMILARITY).
 CC CHAIN 712 770 GAMMA-CTF(59) (BY SIMILARITY).
 CC CHAIN 714 770 GAMMA-CTF(57) (BY SIMILARITY).
 CC
 CC Query Match 100.0%; Score 62; DB 1; Length 770;
 CC Best Local Similarity 100.0%; Pred. No. 0.00062; Gaps 0;
 CC Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC 1 KRQYTSIHGG 11
 CC | | | | | | | | | | | |
 CC Db 724 KRQYTSIHGG 734

RESULT 3

AC A4_HUMAN STANDARD; PRT; 770 AA.
 AC P05067; P09000; P78438; Q13764; Q13778; Q13793; Q16011; Q16014;
 AC Q16019; Q16020; Q9BT38; Q9UCA9; Q9UCB6; Q9UCB8; Q9UCD1; Q9UQ58;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 01-NOV-1991 (Rel. 20, Last sequence update)
 DT 15-NOV-2004 (Rel. 43, Last annotation update)
 DE Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
 DE amyloid protein) (Cerebral vascular amyloid peptide) (CVAP) (Protease
 DE nexin-II) (PN-II) (APPI) (PreA4) (Contains: Soluble APP-alpha (S-APP-
 DE alpha); Soluble APP-beta (S-APP-beta); C99; Beta-amyloid protein 42
 DE (Beta-APP42); Beta-amyloid protein 40 (Beta-APP40); C83; P3(42);
 DE P3(40); Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59);
 DE (Amyloid intracellular domain 59) (AID(59)); Gamma-CTF(57) (Gamma-
 DE secretase C-terminal fragment 57) (Amyloid intracellular domain 57)
 DE (AID(57)); Gamma-CTF(50) (Gamma-secretase C-terminal fragment 50)
 DE (Amyloid intracellular domain 50) (AID(50)); C31].
 GN APP OR A4 OR AD1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM APP695).
 RC TISSUE=Brain;
 RX MEDLINE=87144572; PubMed=2881207;
 RA Kang J., Lemaire H.-G., Unterbeck A., Salbaum J.M., Masters C.L.,
 RA Grzeschik K.-H., Multhaup G., Beyreuther K., Mueller-Hill B.;
 RT "The precursor of Alzheimer's disease amyloid A4 protein resembles a
 RT cell-surface receptor.";
 RL Nature 325:733-736(1987).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM APP751).
 RC TISSUE=Brain;
 RX MEDLINE=88122639; PubMed=2893289;
 RA Ponte P., Gonzalez-Demhitt P., Schilling J., Miller J., Hsu D.,
 RA Greenberg B., Davis K., Wallace W., Lieberburg I., Fuller F.,
 RA Cordell B.;
 RT "A new A4 amyloid mRNA contains a domain homologous to serine
 RT proteinase inhibitors.";
 RL Nature 331:525-527(1988).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM APP695).
 RX MEDLINE=89128427; PubMed=2783775;
 RA Lemaire H.-G., Salbaum J.M., Multhaup G., Kang J., Bayne R.M.,
 RA Unterbeck A., Beyreuther K., Mueller-Hill B.;
 RT "The PreA4(695) precursor protein of Alzheimer's disease A4 amyloid
 RT is encoded by 16 exons.";
 RL Nucleic Acids Res. 17:517-522(1989).
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM APP770).
 RX MEDLINE=90236318; PubMed=2110105;
 RA Yoshikai S.-I., Sasaki H., Doh-Ura K., Furiya H., Sasaki Y.;
 RT "Genomic organization of the human amyloid beta-protein precursor
 RT gene.";

RL Gene 87:257-263(1990).
 RP ERRATUM, AND REVISIONS.
 RA Yoshikai S.-I., Sasaki H., Doh-ura K., Furuya H., Sakaki Y.;
 RL Gene 102:1291-292(1991).
 RN [16]
 RP SEQUENCE FROM N.A. (ISOFORM L-APP733).
 RC TISSUE=Leukocyte;
 RX MEDLINE=92268136; PubMed=1587857;
 RA Koenig G., Moening U., Czech C., Prior R., Banati R.,
 RA Schreier-Gasser U., Bauer J., Masters C.L., Beyreuther K.;
 RT "Identification and differential expression of a novel alternative
 RT splice isoform of the beta A4 amyloid precursor protein (APP) mRNA in
 RT leukocytes and brain microglial cells.";
 RL J. Biol. Chem. 267:10604-10609(1992).
 RN [17]
 RP SEQUENCE FROM N.A. (ISOFORM APP770).
 RX MEDLINE=97263807; PubMed=9108164;
 RA Hattori M., Tsukahara F., Furuhata Y., Tanahashi H., Hirose M.,
 RA Saito M., Tsukuni S., Sakaki Y.;
 RT "A novel method for making nested deletions and its application for
 RT sequencing of a 300 kb region of human APP locus.";
 RL Nucleic Acids Res. 25:1802-1808(1997).
 RN [18]
 RP SEQUENCE FROM N.A. (ISOFORM APP639).
 RC TISSUE=Brain;
 RX MEDLINE=22744650; PubMed=1289342;
 RA Tang K., Wang C., Shen C., Sheng S., Ravid R., Jing N.;
 RT "Identification of a novel alternative splicing isoform of human
 RT amyloid precursor protein gene, APP639.";
 RL Eur. J. Neurosci. 15:102-108(2003).
 RN [19]
 RP SEQUENCE FROM N.A. (ISOFORM APP305).
 RC TISSUE=Pancreas;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Lomuelano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Snailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [10]
 RP SEQUENCE OF 1-10 FROM N.A.

RC TISSUE=Liver;
 RX MEDLINE=99016647; PubMed=3140222;
 RA Schon E.A., Mita S., Sadlock J., Herbert J.;
 RT "A cDNA specifying the human amyloid beta precursor protein (ABPP)
 RT encodes a 95-kDa polypeptide.";
 RL Nucleic Acids Res. 16:9351-9351(1988).
 RN [11]
 RP ERRATUM, AND REVISIONS.
 RA Mita S., Sadlock J., Herbert J., Schon E.A.;
 RL Nucleic Acids Res. 16:11402-11402(1988).
 RN [12]
 RP SEQUENCE OF 1-75 FROM N.A.
 RX MEDLINE=89165870; PubMed=2538123;
 RA La Fauci G., Lahiri D.K., Salton S.R., Robakis N.K.;
 RT "Characterization of the 5'-end region and the first two exons of the
 RT beta-protein precursor gene.";
 RL Biochem. Biophys. Res. Commun. 159:297-304(1989).
 RN [13]
 RP SEQUENCE OF 18-50.
 RC TISSUE=Fibroblast;
 RX MEDLINE=87250462; PubMed=3597385;
 RA van Nostrand W.E., Cunningham D.D.;
 RT "Purification of protease nexin II from human fibroblasts.";
 RL J. Biol. Chem. 262:8508-8514(1987).
 RN [14]
 RP PARTIAL SEQUENCE FROM N.A. (ISOFORM APP751).
 RC TISSUE=Brain;
 RX MEDLINE=89346754; PubMed=2569763;
 RA de Sauvage F., Octave J.N.;
 RT "A novel mRNA of the A4 amyloid precursor gene coding for a possibly
 RT secreted protein.";
 RL Science 245:651-653(1999).
 RN [15]
 RP PARTIAL SEQUENCE FROM N.A. (ISOFORM APP695).
 RC TISSUE=Brain;
 RX MEDLINE=87231971; PubMed=3035574;
 RA Robakis N.K., Ramakrishna N., Wolfe G., Wisniewski H.M.;
 RT "Molecular cloning and characterization of a cDNA encoding the
 RT cerebrovasculature and the neuritic plaque amyloid peptides.";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:4190-4194(1987).
 RN [16]
 RP SEQUENCE OF 286-366 FROM N.A.
 RX MEDLINE=89122640; PubMed=2893290;
 RA Tanzi R.E., McClatchey A.I., Lamperti E.D., Villa-Komaroff L.,
 RA Gusella J.F., Neve R.L.;
 RT "Protease inhibitor domain encoded by an amyloid protein precursor
 RT mRNA associated with Alzheimer's disease.";
 RL Nature 331:528-530(1988).
 RN [17]
 RP SEQUENCE OF 287-367 FROM N.A.
 RX MEDLINE=89122641; PubMed=2893291;
 RA Kitaguchi N., Takahashi Y., Tokushima Y., Shiojiri S., Ito H.;
 RT "Novel precursor of Alzheimer's disease amyloid protein shows
 RT protease inhibitory activity.";
 RL Nature 331:530-532(1988).
 RN [18]
 RP SEQUENCE OF 507-770 FROM N.A.

RC TISSUE=Brain cortex;
RX MEDLINE=88124954; PubMed=2893379;
RA Zain S.B., Salim M., Chou W.G., Sajdel-Sulkowska E.M., Majocha R.E.,
RA Marotta C.A.;
RT "Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer
RT disease brain: coding and noncoding regions of the fetal precursor
RT mRNA are expressed in the cortex.";
RL Proc. Natl. Acad. Sci. U.S.A. 85:929-933(1988).
RN [19]
RP SEQUENCE OF 523-555, AND COLLAGEN-BINDING DOMAIN.
RX MEDLINE=96139497; PubMed=8576160;
RA Behner D., Resse L., Masters C.L., Multhaup G.;
RT "Regulation of amyloid protein precursor (APP) binding to collagen and
RT mapping of the binding sites on APP and collagen type I.";
RL J. Biol. Chem. 271:1613-1620(1996).
RN [20]
RP SEQUENCE OF 655-737 FROM N.A., AND VARIANTS AD PHE-717; AD ILE-717
RP AND AD GLY-717.
RX MEDLINE=93236601; PubMed=8476439;
RA Derman R.B., Rosenczwaig R., Miller D.L.;
RT "A system for studying the effect(s) of familial Alzheimer disease
RT mutations on the processing of the beta-amyloid peptide precursor.";
RL Biochem. Biophys. Res. Commun. 192:96-103(1993).
RN [21]
RP SEQUENCE OF 656-737 FROM N.A.
RX MEDLINE=89392030; PubMed=2675937;
RA Johnstone E.M., Chaney M.O., Moore R.E., Ward K.E., Norris F.H.,
RA Little S.P.;
RT "Alzheimer's disease amyloid peptide is encoded by two exons and shows
RT similarity to soybean trypsin inhibitor.";
RL Biochem. Biophys. Res. Commun. 163:1248-1255(1989).
RN [22]
Query Match 100.0%; Score 62; DB 1; Length 770;
Best Local Similarity 100.0%; Pred. No. 0.00062;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KKQYTSIHGG 11
DB 724 KKQYTSIHGG 734
|||||
RESULT 4
A4 MACFA STANDARD; PRT; 770 AA.
AC P53601; Q95KN7;
DT 01-OCT-1996 (Rel. 34, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
DE amyloid protein homolog) [Contains: Soluble APP-alpha (S-APP-alpha);
DE Soluble APP-beta (S-APP-beta); C99; Beta-amyloid protein 42 (Beta-
DE APP42); Beta-amyloid protein 40 (Beta-APP40); C83; P3(42); P3(40);
DE Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-CTF(57)
DE (Gamma-secretase C-terminal fragment 57); Gamma-CTF(50) (Gamma-
DE secretase C-terminal fragment 50); C31].
GN APP.

OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9541;
[1]
RP SEQUENCE FROM N.A. (ISOFORMS APP695 AND APP770).
RC TISSUE=Cerebellum;
RX MEDLINE=91273117; PubMed=1905108;
RA Podlisky M.B., Tolan D.R., Selkoe D.J.;
RT "Homology of the amyloid beta protein precursor in monkey and human
RT supports a primate model for beta amyloidosis in Alzheimer's
RT disease.";
RL Am. J. Pathol. 138:1423-1435(1991).
CC -!- FUNCTION: Functions as a cell surface receptor and performs
CC physiological functions on the surface of neurons relevant to
CC neurite growth, neuronal adhesion and axonogenesis. Involved in
CC cell motility and transcription regulation through protein-protein
CC interactions (By similarity). Can promote transcription activation
CC through binding to APBB1/Tip60 and inhibit Notch signaling through
CC interaction with Numb (By similarity). Couples to apoptosis-
CC inducing pathways such as those mediated by G(I) and JIP (By
CC similarity). Inhibits G(I) alpha ATPase activity (By similarity).
CC Acts as a kinesin I membrane receptor, mediating the axonal
CC transport of beta-secretase and Presenilin 1 (By similarity). May
CC be involved in copper homeostasis/oxidative stress through copper
CC ion reduction. In vitro, copper-metalated APP induces neuronal
CC death directly or is potentiated through Cu(II)-mediated low-
CC density lipoprotein oxidation (By similarity). Can regulate
CC neurite outgrowth through binding to components of the
CC extracellular matrix such as heparin and collagen I and IV (By
CC similarity). The splice isoforms that contain the BPT1 domain
CC possess protease inhibitor activity (By similarity).
CC -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
CC with metal-reducing activity. Bind transient metals such as
CC copper, zinc and iron (By similarity).
CC -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
CC peptides, including C31, are potent enhancers of neuronal
CC apoptosis (By similarity).
CC -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
CC cytoplasmic proteins, including APBB family members, the APPA
CC family, MAPK8IP1, and SHC1, Numb and Dab1 (By similarity). Binding
CC to Dab1 inhibits its serine phosphorylation (By similarity). Also
CC interacts with GPCR-like protein BPP, FRL1, APPBP1, IBL, KNS2
CC (via its TPR domains) (By similarity), APPBP2 (via Bass) and DDB1.
CC In vitro, it binds MAPT via the MT-binding domains (By
CC similarity). Associates with microtubules in the presence of ATP
CC and in a kinesin-dependent manner (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
CC protein that rapidly becomes internalized via clathrin-coated
CC pits. During maturation, the immature APP (N-glycosylated in the
CC endoplasmic reticulum) moves to the Golgi complex where complete
CC maturation occurs (O-glycosylated and sulfated). After alpha-
CC secretase cleavage, soluble APP is released into the extracellular
CC space and the C-terminal is internalized to endosomes and
CC lysosomes. Some APP accumulates in secretory transport vesicles
CC leaving the late Golgi compartment and returns to the cell

surface. Gamma-CTF(59) peptide is located to both the cytoplasm and nuclei of neurons (By similarity).

-|- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;
Comment=Additional isoforms seem to exist;
Name=APP770;
IsoId=PS3601-1; Sequence=Displayed;
Name=APP695;
IsoId=PS3601-2; Sequence=VSP_000010; VSP_000011;
DOMAIN: The basolateral sorting signal (BaSS) is required for sorting of membrane proteins to the basolateral surface of epithelial cells (By similarity).

-|- DOMAIN: The NPXY sequence motif found in many tyrosine-phosphorylated proteins is required for the specific binding of the PID domain. However additional amino acids either N- or C-terminal to the NPXY motif are often required for complete interaction. The PID domain-containing proteins which bind APP require the YENPTY motif for full interaction. These interactions are independent of phosphorylation on the terminal tyrosine residue. The NPXY site is also involved in clathrin-mediated endocytosis (By similarity).

-|- PTM: Proteolytically processed under normal cellular conditions. Cleavage by alpha-secretase or alternatively by beta-secretase leads to generation and extracellular release of soluble APP peptides, S-APP-alpha and S-APP-beta, respectively, and the retention of corresponding membrane-anchored C-terminal fragments, C83 and C99. Subsequent processing of C83 by gamma-secretase yields P3 peptides. This is the major secretory pathway and is nonamyloidogenic. Alternatively, presenilin/nicastrin-mediated gamma-secretase processing of C99 releases the amyloid beta proteins, amyloid-beta 40 (Abeta40) and amyloid-beta 42 (Abeta42), major components of amyloid plaques, and the cytotoxic C-terminal fragments, gamma-CTF(50), gamma-CTF(57), and gamma-CTF(59) (By similarity).

-|- PTM: Proteolytically cleaved by caspases during neuronal apoptosis (By similarity). Cleavage at Asp-739 by either caspase-3, -8 or -9 results in the production of the neurotoxic C31 peptide and the increased production of beta-amyloid peptides (By similarity).

-|- PTM: N- and O-glycosylated (By similarity).

-|- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and serine residues is neuron-specific. Phosphorylation can affect APP processing, neuronal differentiation and interaction with other proteins (By similarity).

-|- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and zinc, can induce histidine-bridging between beta-amyloid molecules resulting in beta-amyloid-metal aggregates (By similarity). Extracellular zinc-binding increases binding of heparin to APP and inhibits collagen-binding (By similarity).

-|- SIMILARITY: Belongs to the APP family.

-|- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.

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EMBL; M58727; AAA36829.1; -;
EMBL; M58726; AAA36828.1; -;
HSSP; P03067; IAAp.
InterPro; IPR008155; A4_APP.
InterPro; IPR008154; A4_extra.
InterPro; IPR001255; Beta-APP.
InterPro; IPR002223; Kunitz_BPTI.
Pfam; PF02177; A4_EXTRA; 1.
Pfam; PF03494; Beta-APP; 1.
Pfam; PF00014; Kunitz_BPTI; 1.
PRINTS; PR00203; AMYLOIDA4.
PRINTS; PR00759; BASIOPTASE.
ProDom; PD000222; Kunitz_BPTI; 1.
SMART; SM00066; A4_EXTRA; 1.
SMART; SM00131; X0; 1.
PROSITE; PS00319; A4_EXTRA; 1.
PROSITE; PS00320; A4_INTRA; 1.
PROSITE; PS00280; BPTI_KUNITZ_1; 1.
PROSITE; PS00279; BPTI_KUNITZ_2; 1.
Apoptosis; Endocytosis; Cell adhesion; Serine protease inhibitor;
Coated pits; Neurons; Heparin-binding; Metal-binding; Copper; Iron;
Zinc; Signal; Transmembrane; Glycoprotein; Phosphorylation;
Proteoglycan; Alternative splicing; Amyloid.
FT SIGNAL 1 17
FT CHAIN 18 770 AMYLOID BETA A4 PROTEIN.
FT CHAIN 18 687 SOLUBLE APP-ALPHA (POTENTIAL).
FT CHAIN 18 671 SOLUBLE APP-BETA (POTENTIAL).
FT CHAIN 672 770 C99 (POTENTIAL).
FT CHAIN 672 713 BETA-AMYLOID PROTEIN 42 (POTENTIAL).
FT CHAIN 672 711 BETA-AMYLOID PROTEIN 40 (POTENTIAL).
FT CHAIN 688 770 C83 (POTENTIAL).
FT CHAIN 688 713 P3(42) (POTENTIAL).
FT CHAIN 688 711 P3(40) (POTENTIAL).
FT CHAIN 712 770 GAMMA-CTF(39) (POTENTIAL).
FT CHAIN 714 770 GAMMA-CTF(37) (POTENTIAL).
FT CHAIN 721 770 GAMMA-CTF(50) (POTENTIAL).
FT CHAIN 740 770 C31 (POTENTIAL).
FT DOMAIN 18 699 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 700 723 POTENTIAL.
FT DOMAIN 724 770 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 96 110 HEPARIN-BINDING (BY SIMILARITY).
FT DOMAIN 181 188 ZINC-BINDING (BY SIMILARITY).
FT DOMAIN 291 341 BPTI/KUNITZ INHIBITOR.
FT DOMAIN 391 423 HEPARIN-BINDING (BY SIMILARITY).
FT DOMAIN 491 522 HEPARIN-BINDING (BY SIMILARITY).
FT DOMAIN 523 540 COLLAGEN-BINDING (BY SIMILARITY).
FT DOMAIN 732 751 INTERACTION WITH G(O)-ALPHA (BY SIMILARITY).
FT DOMAIN 230 260 ASP/GLU-RICH (ACIDIC).
FT DOMAIN 274 280 POLY-THR.
FT SITE 144 REQUIRED FOR COPPER(II) REDUCTION (BY SIMILARITY).
FT ACT SITE 301 REACTIVE BOND (BY SIMILARITY).
FT SITE 671 CLEAVAGE (BY BETA-SECRETASE) (BY SIMILARITY).
FT 672

FT SITE 672 673 CLEAVAGE (BY CASPASE-6) (BY SIMILARITY).
 FT SITE 687 688 CLEAVAGE (BY ALPHA-SECRETASE)
 FT SITE 704 704 IMPLICATED IN FREE RADICAL PROPAGATION
 FT SITE 706 706 INVOLVED IN OXIDATIVE REACTIONS
 FT SITE 711 712 CLEAVAGE (BY GAMMA-SECRETASE; SITE 1)
 FT SITE 713 714 CLEAVAGE (BY GAMMA-SECRETASE; SITE 2)
 FT SITE 720 721 CLEAVAGE (BY GAMMA-SECRETASE; SITE 3)
 FT SITE 724 734 BASOLATERAL SORTING SIGNAL
 FT SITE 739 740 CLEAVAGE (BY CASPASES-3,-6,-8 OR -9)

Query Match 100.0%; Score 62; DB 1; Length 770;
 Best Local Similarity 100.0%; Pred. No. 0.00062;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKQYTSIHG 11
 |||||
 Db 724 KKQYTSIHG 734

RESULT 5

A4_MOUSE STANDARD; PRT; 770 AA.
 AC P12023; P97487; P97942; Q99K32;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
 DE amyloid protein homolog) (Amyloidogenic glycoprotein) (AG) (Contains:
 DE Soluble APP-alpha (S-APP-alpha); Soluble APP-beta (S-APP-beta); C99
 DE (APP-C99); Beta-amyloid protein 42 (Beta-APP42); Beta-amyloid protein
 DE 40 (Beta-APP40); C83; P3(42); P3(40); Gamma-CTF(59) (Gamma-secretase
 DE C-terminal fragment 59) (Amyloid intracellular domain 59) (AID(59))
 DE (APP-C59); Gamma-CTF(57) (Gamma-secretase C-terminal fragment 57)
 DE (Amyloid intracellular domain 57) (AID(57)) (APP-C57); Gamma-CTF(50)
 DE (Gamma-secretase C-terminal fragment 50) (Amyloid intracellular domain
 DE 50) (AID(50)); C31).

GN APP.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM APP695).
 RC TISSUE=Brain;
 RX MEDLINE=88106489; PubMed=3322280;
 RA Yamada T., Sasaki H., Furuya H., Miyata T., Goto I., Sakaki Y.;
 RT "Complementary DNA for the mouse homolog of the human amyloid beta
 RT protein precursor.";
 RL Biochem. Biophys. Res. Commun. 149:665-671(1987).

RN [2]
 RP REVISIONS.
 RA Yamada T.;
 RL Submitted (VAR-1988) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM APP695).
 RC STRAIN=BA1B/c; TISSUE=Brain;
 RX MEDLINE=92096498; PubMed=1736177;
 RA de Strooper B., van Leuven F., van den Bergh H.;
 RT "The amyloid beta protein precursor or proteinase nexin II from mouse
 RT is closer related to its human homolog than previously reported.";
 RL Biochim. Biophys. Acta 1129:141-143(1991).
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM APP695).
 RC STRAIN=SAMP8; TISSUE=Hippocampus;
 RX MEDLINE=21130647; PubMed=11235921;
 RA Kumar V.B., Vyas K., Franko M., Choudhary V., Buddhiraju C.,
 RA Alvarez J., Morley J.E.;
 RT "Molecular cloning, expression, and regulation of hippocampal amyloid
 RT precursor protein of senescence accelerated mouse (SAMP8).";
 RL Biochem. Cell Biol. 79:57-67(2001).
 RN [5]
 RP SEQUENCE OF 1-19 FROM N.A.
 RX MEDLINE=92209998; PubMed=1555768;
 RA Izumi R., Yamada T., Yoshikai S.I., Sasaki H., Hattori M.,
 RA Sakai Y.;
 RT "Positive and negative regulatory elements for the expression of the
 RT Alzheimer's disease amyloid precursor-encoding gene in mouse.";
 RL Gene 112:189-195(1992).
 RN [6]
 RP PARTIAL SEQUENCE FROM N.A. (ISOFORM APP770).
 RC TISSUE=Breast tumor;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueudin T.B., Teshiguchi S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [7]
 RP SEQUENCE OF 281-380 FROM N.A., AND ALTERNATIVE SPLICING.
 RC TISSUE=Brain, and Kidney;

RX MEDLINE=89149813; PubMed=2493250;
 RA Yamada T., Sasaki H., Dohura K., Goto I., Sakaki Y.;
 RT "Structure and expression of the alternatively-spliced forms of mRNA
 for the mouse homolog of Alzheimer's disease amyloid beta protein
 precursor";
 RL Biochem. Biophys. Res. Commun. 158:906-912(1989).
 RN [18]
 RP SEQUENCE OF 289-364 FROM N.A.
 RC STRAIN=CD-1; TISSUE=Placenta;
 RX MEDLINE=89345111; PubMed=2569710;
 RA Fukuchi K., Martin G.M., Deeb S.S.;
 RT "Sequence of the protease inhibitor domain of the A4 amyloid protein
 precursor of *Mus domesticus*";
 RL Nucleic Acids Res. 17:5396-5396(1989).
 RN [19]
 RP SEQUENCE OF 656-737 FROM N.A.
 RC STRAIN=129/Sv;
 RA Wragg M.A., Busfield F., Duff K., Korenblat K., Capocchi M.,
 RA Loring J.F., Goate A.M.;
 RT "Introduction of six mutations into the mouse genome using 'Hit and
 Run' gene-targeting: introduction of familial Alzheimer's disease
 mutations into the mouse amyloid precursor protein gene and
 humanization of the A-beta fragment";
 RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
 RN [10]
 RP TISSUE SPECIFICITY OF ALTERNATIVE SPLICED FORMS.
 RX MEDLINE=93287808; PubMed=8510506;
 RA Sola C., Mengod G., Ghetti B., Palacios J.M., Triarhou L.C.;
 RT "Regional distribution of the alternatively spliced isoforms of beta
 APP RNA transcript in the brain of normal, heterozygous and
 homozygous weaver mutant mice as revealed by in situ hybridization
 histochemistry";
 RL Brain Res. Mol. Brain Res. 17:340-346(1993).
 RN [11]
 RP INTERACTION WITH KNS2.
 RX MEDLINE=21010507; PubMed=11144355;
 RA Kamal A., Stokin G.S., Yang Z., Xia C.-K., Goldstein L.S.;
 RT "Axonal transport of amyloid precursor protein is mediated by direct
 binding to the kinesin light chain subunit of kinesin-I";
 RL Neuron 28:449-459(2000).
 RN [12]
 RP C-TERMINAL PROTEIN-PROTEIN INTERACTIONS, AND MUTAGENESIS OF TYR-728;
 RP THR-743; TYR-757; ASN-759 AND TYR-762.
 RX MEDLINE=21408156; PubMed=11517249;
 RA Matsuda S., Yasukawa T., Honma Y., Ito Y., Niikura T., Hiraki T.,
 RA Hirai S., Ohno S., Kita Y., Kawasumi M., Koyama K., Yamamoto T.,
 RA Kyriakis J.M., Nishimoto I.;
 RT "C-Jun N-terminal kinase (JNK)-interacting protein-1b/Islet-brain-1
 scaffolds Alzheimer's amyloid precursor protein with JNK";
 RL J. Neurosci. 21:6597-6607(2001).
 RN [13]
 RP INTERACTION WITH MAPK8IP1, AND PHOSPHORYLATION.
 RX MEDLINE=22028091; PubMed=11912189;
 RA Taru H., Iijima K.-I., Hase M., Kirino Y., Yagi Y., Suzuki T.;
 RT "Interaction of Alzheimer's beta-amyloid precursor family proteins
 with scaffold proteins of the JNK signaling cascade";
 RL J. Biol. Chem. 277:20070-20078(2002).

RN INTERACTION OF CTF PEPTIDES WITH NUMB.
 RP MEDLINE=22008109; PubMed=12011466;
 RA Roncarati R., Sestan N., Scheinfeld M.H., Berechid B.E., Lopez P.A.,
 RA Maucci O., McGlade J.C., Rakic P., D'Adamo L.;
 RT "The gamma-secretase-generated intracellular domain of beta-amyloid
 precursor protein binds Numb and inhibits Notch signaling";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:7102-7107(2002).
 RN [15]
 RP GAMMA-SECRETASE PROCESSING, AND INTERACTION WITH APBB1.
 RX MEDLINE=21437805; PubMed=11553691;
 RA Cupers P., Orlans I., Craessaerts K., Annaert W., De Strooper B.;
 RT "The amyloid precursor protein (APP)-cytoplasmic fragment generated by
 gamma-secretase is rapidly degraded but distributes partially in a
 nuclear fraction of neurons in culture";
 RL J. Neurochem. 78:1168-1178(2001).
 CC -|- FUNCTION: Functions as a cell surface receptor and performs
 physiological functions on the surface of neurons relevant to
 neurite growth, neuronal adhesion and axonogenesis. Involved in
 cell motility and transcription regulation through protein-protein
 interactions. Can promote transcription activation through binding
 to APBB1/Tip60 and inhibit Notch signaling through interaction
 with Numb. Couples to apoptosis-inducing pathways such as those
 mediated by G(O) and JIP. Inhibits G(O) alpha Affase activity (By
 similarity). Acts as a kinesin I membrane receptor, mediating the
 axonal transport of beta-secretase and presenilin 1. May be
 involved in copper homeostasis/oxidative stress through copper ion
 reduction. Can regulate neurite outgrowth through binding to
 components of the extracellular matrix such as heparin and
 collagen I and IV (By similarity). The splice isoforms that
 contain the BPTI domain possess protease inhibitor activity (By
 similarity).
 CC -|- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
 with metal-reducing activity. Bind transient metals such as
 copper, zinc and iron. Rat and mouse beta-amyloid peptides bind
 only weakly transient metals and have little reducing activity due
 to substitutions of transient metal chelating residues. Beta-APP42
 may activate mononuclear phagocytes in the brain and elicit
 inflammatory responses. Promotes both tau aggregation and TPK II-
 mediated phosphorylation (By similarity).
 CC -|- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
 peptides, including C31, are potent enhancers of neuronal
 apoptosis.
 CC -|- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
 cytoplasmic proteins, including APBB family members, the APBA
 family, MAPK8IP1, SHC1, Numb and Dab1. Binding to Dab1 inhibits
 its serine phosphorylation. Also interacts with GPCR-like protein
 BPP, FPR1, APPB21, IBL, KNS2 (via its TPR domains), APPB2 (via
 BASS) and DDB1 (By similarity). In vitro, it binds NAPT via the
 NT-binding domains (By similarity). Associates with microtubules
 in the presence of APP and in a kinesin-dependent manner (By
 similarity). Interacts, through a C-terminal domain, with GNAO1
 (By similarity). Amyloid beta-42 binds CHRNA7 in hippocampal
 neurons (By similarity). Beta-amyloid associates with HADH2 (By
 similarity).
 CC -|- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
 protein that rapidly becomes internalized via clathrin-coated

CC pits. During maturation, the immature APP (N-glycosylated in the
CC endoplasmic reticulum) moves to the Golgi complex where complete

Query Match 100.0%; Score 62; DB 1; Length 770;
Best Local Similarity 100.0%; Pred. No. 0.00062;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKQYTSIHG 11
|||||||
Db 724 KKQYTSIHG 734

RESULT 6

A4_PIG STANDARD; PRT; 770 AA.

AC P79307; Q29023; Q9TU10;
DT 01-NOV-1997 (Rel. 35, Created)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
DE amyloid protein homolog) [Contains: Soluble APP-alpha (S-APP-alpha);
DE Soluble APP-beta (S-APP-beta); C99; Beta-amyloid protein 42 (Beta-
DE APP42); Beta-amyloid protein 40 (Beta-APP40); C83; P3(42); P3(40);
DE Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-CTF(57)
DE (Gamma-secretase C-terminal fragment 57); Gamma-CTF(50) (Gamma-
DE secretase C-terminal fragment 50); C31].
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Kimura A., Takahashi T.;
RT "Amyloid precursor protein 770.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 1-136 FROM N.A.
RC TISSUE=Small intestine;
RA Winteroe A.K., Fredholm M.;
RT "Evaluation and characterization of a porcine small intestine cDNA
RT library.";
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 667-723 FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=92017079; PubMed=1656157;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -!- FUNCTION: Functions as a cell surface receptor and performs
CC physiological functions on the surface of neurons relevant to
CC neurite growth, neuronal adhesion and axonogenesis. Involved in
CC cell mobility and transcription regulation through protein-protein
CC interactions (By similarity). Can promote transcription activation
CC through binding to APPB1/Tip60 and inhibit Notch signaling through

interaction with Numb (By similarity). Couples to apoptosis-
inducing pathways such as those mediated by G10 and JIP (By
similarity). Inhibits G10 alpha Atase activity (By similarity).
Acts as a kinesin I membrane receptor, mediating the axonal
transport of beta-secretase and presenilin 1 (By similarity). May
be involved in copper homeostasis/oxidative stress through copper
ion reduction (By similarity). In vitro, copper-metalated APP
induces neuronal death directly or is potentiated through Cu(II)-
mediated low-density lipoprotein oxidation (By similarity). Can
regulate neurite outgrowth through binding to components of the
extracellular matrix such as heparin and collagen I and IV (By
similarity).
CC -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
CC with metal-reducing activity. Bind transient metals such as
CC copper, zinc and iron (By similarity).
CC -!- FUNCTION: The gamma-Ctf peptides as well as the caspase-cleaved
CC peptides, including C31, are potent enhancers of neuronal
CC apoptosis (By similarity).
CC -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
CC cytoplasmic proteins, including APPB family members, the APPA
CC family, MAPKBP1, and SHC1, Numb and Dab1 (By similarity). Binding
CC to Dab1 inhibits its serine phosphorylation (By similarity). Also
CC interacts with GPCR-like protein EPP, FPL1, APPB1, Ibl, KMS2
CC (via its TPR domains) (By similarity), APPB2 (via Bass) and DBL1.
CC In vitro, it binds MAPT via the MT-binding domains (By
CC similarity). Associates with microtubules in the presence of ATP
CC and in a kinesin-dependent manner (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
CC protein that rapidly becomes internalized via clathrin-coated
CC pits. During maturation, the immature APP (N-glycosylated in the
CC endoplasmic reticulum) moves to the Golgi complex where complete
CC maturation occurs (O-glycosylated and sulfated). After alpha-
CC secretase cleavage, soluble APP is released into the extracellular
CC space and the C-terminal is internalized to endosomes and
CC lysosomes. Some APP accumulates in secretory transport vesicles
CC leaving the late Golgi compartment and returns to the cell
CC surface. Gamma-CTF(53) peptide is located to both the cytoplasm
CC and nuclei of neurons (By similarity).
CC -!- DOMAIN: The basolateral sorting signal (BASS) is required for
CC sorting of membrane proteins to the basolateral surface of
CC epithelial cells (By similarity).
CC -!- DOMAIN: The NPXY sequence motif found in many tyrosine-
CC phosphorylated proteins is required for the specific binding of
CC terminal to the NPXY motif are often required for complete
CC interaction. The PID domain-containing proteins which bind APP
CC require the YENPTY motif for full interaction. These interactions
CC are independent of phosphorylation on the terminal tyrosine
CC residue. The NPXY site is also involved in clathrin-mediated
CC endocytosis (By similarity).
CC -!- PTM: Proteolytically processed under normal cellular conditions.
CC Cleavage by alpha-secretase or alternatively by beta-secretase
CC leads to generation and extracellular release of soluble APP
CC peptides, S-APP-alpha and S-APP-beta, respectively, and the
CC retention of corresponding membrane-anchored C-terminal fragments,
CC C83 and C99. Subsequent processing of C83 by gamma-secretase
CC yields P3 peptides. This is the major secretory pathway and is

nonamyloidogenic. Alternatively, presenilin/nicastrin-mediated gamma-secretase processing of C99 releases the amyloid beta proteins, amyloid-beta 40 (Aβ40) and amyloid-beta 42 (Aβ42), major components of amyloid plaques, and the cytotoxic C-terminal fragments, gamma-CTF(30), gamma-CTF(57) and gamma-CTF(59) (By similarity).

-!- PM: Proteolytically cleaved by caspases during neuronal apoptosis (By similarity). Cleavage at Asp-739 by either caspase-3, -8 or -9 results in the production of the neurotoxic C31 peptide and the increased production of beta-amyloid peptides (By similarity).

-!- PM: N- and O-glycosylated (By similarity).

-!- PM: Phosphorylation in the C-terminal on tyrosine, threonine and serine residues is neuron-specific. Phosphorylation can affect APP processing, neuronal differentiation and interaction with other proteins (By similarity).

-!- PM: Extracellular binding and reduction of copper, results in a corresponding oxidation of Cys-144 and Cys-158, and the formation of a disulfide bond (By similarity).

-!- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and zinc, can induce histidine-bridging between beta-amyloid molecules resulting in beta-amyloid-metal aggregates (By similarity). Extracellular zinc-binding increases binding of heparin to APP and inhibits collagen-binding (By similarity).

-!- SIMILARITY: Belongs to the APP family.

-!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.

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EMBL; AB032550; BAA84580.1; -.
EMBL; Z84022; CAB06313.1; -.
EMBL; X56127; CAA39592.1; -.
HSSP; P05067; 1AAP.
InterPro; IPR008155; A4_APP.
InterPro; IPR008154; A4_extra.
InterPro; IPR002223; Kunitz_BPTI.
Pfam; PF02177; A4_EXTRA; 1.
PRINTS; PR00203; AMYLOIDA4.
ProDom; PD00222; Kunitz_BPTI; 1.
SMART; SM00006; A4_EXTRA; 1.
SMART; SM00131; KUJ; 1.
PROSITE; PS00319; A4_EXTRA; 1.
PROSITE; PS00320; A4_INTRA; 1.
PROSITE; PS00280; BPTI_KUNITZ_1; 1.
PROSITE; PS00279; BPTI_KUNITZ_2; 1.
KW Apoptosis; Endocytosis; Cell adhesion; Serine protease inhibitor; Coated pits; Neurone; Heparin-binding; Metal-binding; Copper; Iron;
KW Zinc; Signal; Transmembrane; Glycoprotein; Phosphorylation;
KW Amyloid.
FT SIGNAL 1 17 BY SIMILARITY.
FT CHAIN 18 770 AMYLOID BETA A4 PROTEIN.

FT CHAIN	18	687	18	687	FT CHAIN	18	687	SOLUBLE APP-ALPHA (POTENTIAL).
FT CHAIN	18	671	18	671	FT CHAIN	18	671	SOLUBLE APP-BETA (POTENTIAL).
FT CHAIN	672	770	672	770	FT CHAIN	672	770	C99 (BY SIMILARITY).
FT CHAIN	672	713	672	713	FT CHAIN	672	713	BETA-AMYLOID PROTEIN 42 (BY SIMILARITY).
FT CHAIN	672	711	672	711	FT CHAIN	672	711	BETA-AMYLOID PROTEIN 40 (BY SIMILARITY).
FT CHAIN	688	770	688	770	FT CHAIN	688	770	C83 (BY SIMILARITY).
FT CHAIN	688	713	688	713	FT CHAIN	688	713	F3(42) (BY SIMILARITY).
FT CHAIN	688	711	688	711	FT CHAIN	688	711	F3(40) (BY SIMILARITY).
FT CHAIN	712	770	712	770	FT CHAIN	712	770	GAMMA-CTF(59).
FT CHAIN	714	770	714	770	FT CHAIN	714	770	GAMMA-CTF(57).
FT CHAIN	721	770	721	770	FT CHAIN	721	770	GAMMA-CTF(50) (BY SIMILARITY).
FT CHAIN	740	770	740	770	FT CHAIN	740	770	C31 (DURING APOPTOSIS) (BY SIMILARITY).
FT DOMAIN	18	699	18	699	FT DOMAIN	18	699	EXTRACELLULAR (POTENTIAL).
FT TRANSMEM	700	723	700	723	FT TRANSMEM	700	723	POTENTIAL.
FT DOMAIN	724	770	724	770	FT DOMAIN	724	770	CYTOPLASMIC (POTENTIAL).
FT DOMAIN	96	110	96	110	FT DOMAIN	96	110	HEPARIN-BINDING (BY SIMILARITY).
FT DOMAIN	135	155	135	155	FT DOMAIN	135	155	COPPER-BINDING (BY SIMILARITY).
FT DOMAIN	181	188	181	188	FT DOMAIN	181	188	ZINC-BINDING (BY SIMILARITY).
FT DOMAIN	291	341	291	341	FT DOMAIN	291	341	BPTI/KUNITZ INHIBITOR.
FT DOMAIN	391	423	391	423	FT DOMAIN	391	423	HEPARIN-BINDING (BY SIMILARITY).
FT DOMAIN	491	522	491	522	FT DOMAIN	491	522	HEPARIN-BINDING (BY SIMILARITY).
FT DOMAIN	523	540	523	540	FT DOMAIN	523	540	COLLAGEN-BINDING (BY SIMILARITY).
FT DOMAIN	732	751	732	751	FT DOMAIN	732	751	INTERACTION WITH G10-ALPHA (BY SIMILARITY).
FT DOMAIN	230	260	230	260	FT DOMAIN	230	260	ASP/GLU-RICH (ACIDIC).
FT DOMAIN	274	280	274	280	FT DOMAIN	274	280	POLY-THR.
FT SITE	144	144	144	144	FT SITE	144	144	REQUIRED FOR COPPER(II) REDUCTION (BY SIMILARITY).
FT ACT_SITE	301	302	301	302	FT ACT_SITE	301	302	REACTIVE BOND (BY SIMILARITY).
FT SITE	671	672	671	672	FT SITE	671	672	CLEAVAGE (BY BETA-SECRETASE) (BY SIMILARITY).
FT SITE	672	673	672	673	FT SITE	672	673	CLEAVAGE (BY CASPASE-6) (BY SIMILARITY).
FT SITE	687	688	687	688	FT SITE	687	688	CLEAVAGE (BY ALPHA-SECRETASE) (BY SIMILARITY).
FT SITE	704	704	704	704	FT SITE	704	704	IMPLICATED IN FREE RADICAL PROPAGATION (BY SIMILARITY).
FT SITE	706	706	706	706	FT SITE	706	706	INVOLVED IN OXIDATIVE REACTIONS (BY SIMILARITY).
FT SITE	711	712	711	712	FT SITE	711	712	CLEAVAGE (BY GAMMA-SECRETASE; SITE 1) (BY SIMILARITY).
FT SITE	713	714	713	714	FT SITE	713	714	CLEAVAGE (BY GAMMA-SECRETASE; SITE 2) (BY SIMILARITY).
FT SITE	720	721	720	721	FT SITE	720	721	CLEAVAGE (BY GAMMA-SECRETASE; SITE 3) (BY SIMILARITY).

Query Match 100.0%; score 62; DB 1; length 770;
Best Local Similarity 100.0%; Pred. No. 0.00062;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKQYTSIHG 11
|||||
Db 724 KKQYTSIHG 734

RESULT 7
A4_RAT
ID A4_RAT
AC P08592;

DT 01-AUG-1988 (Rel. 08, 'Created)

DT 01-DEC-1992 (Rel. 24, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Amyloid beta A4 protein precursor (APP) (Alzheimer's disease amyloid

DE protein homolog) (Amyloidogenic glycoprotein) (AG) [Contains: Soluble

DE APP-alpha (S-APP-alpha); Soluble APP-beta (S-APP-beta); C99; Beta-

DE amyloid protein 42 (Beta-APP42); Beta-amyloid protein 40 (Beta-APP40);

DE C83; P3(42); P3(40); Gamma-CTF(59) (Gamma-secretase C-terminal

DE fragment 59); Gamma-CTF(57) (Gamma-secretase C-terminal fragment 57);

DE Gamma-CTF(50) (Gamma-secretase C-terminal fragment 50); C31].

GN APP.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A. (ISOFORM APP695).

RC TISSUE=Brain;

RX MEDLINE=88312583; PubMed=2900758;

RA Shivers B.D., Hilbich C., Multhaup G., Salbaum J.M., Beyreuther K.,

RA Seeburg P.H.; Hilbich C., Multhaup G., Salbaum J.M., Beyreuther K.,

RT "Alzheimer's disease amyloidogenic glycoprotein: expression pattern

RT in rat brain suggests a role in cell contact.";

RL EXO J. 7:1365-1370(1988).

RN [2]

RP SEQUENCE OF 289-364 FROM N.A.

RC TISSUE=Liver;

RX MEDLINE=89183625; PubMed=2648331;

RA Kang J., Mueller-Hill B.;

RT "The sequence of the two extra exons in rat preA4.";

RL Nucleic Acids Res. 17:2130-2130(1989).

RN [3]

RP SEQUENCE OF 720-730, AND MASS SPECTROMETRY.

RX MEDLINE=21443797; PubMed=11483588;

RA Gu Y., Misonou H., Sato T., Dohmae N., Takio K., Ihara Y.;

RT "Distinct intramembrane cleavage of the beta-amyloid precursor protein

RT family resembling gamma-secretase-like cleavage of Notch.";

RL J. Biol. Chem. 276:35235-35238(2001).

RN [4]

RP ALTERNATIVE SPLICING.

RX MEDLINE=96187032; PubMed=8624099;

RA Sandbrink R., Masters C.L., Beyreuther K.;

RT "APP gene family. Alternative splicing generates functionally related

RT isoforms.";

RL Ann. N.Y. Acad. Sci. 777:281-287(1996).

RN [5]

RP TISSUE SPECIFICITY OF APPICAN.

RX MEDLINE=95263526; PubMed=7744833;

RA Shioi J., Pangalos M.N., Ribellino J.A., Vassilacopoulou D.,

RA Mytilineou C., Margolis R.U., Robakis N.K.;

RT "The Alzheimer amyloid precursor proteoglycan (appican) is present in

RT brain and is produced by astrocytes but not by neurons in primary

RT neural cultures.";

RL J. Biol. Chem. 270:11839-11844(1995).

RN [6]

RP TISSUE SPECIFICITY OF ISOFORMS.

RX MEDLINE=97150061; PubMed=896634;

RA Sandbrink R., Monning U., Masters C.L., Beyreuther K.;

RT "Expression of the APP gene family in brain cells, brain development

RT and aging.";

RL Gerontology 43:119-131(1997).

RN [7]

RP INTERACTION WITH DDB1, AND MUTAGENESIS OF TYR-757; ASN-759 AND

RP TYR-762.

RX MEDLINE=98127916; PubMed=9930726;

RA Watanabe T., Sukegawa J., Tomita S., Iijima K.-I., Oguchi S.,

RA Suzuki T., Nairn A.C., Greengard P.;

RT "A 127-kDa protein (UV-DB) binds to the cytoplasmic domain of the

RT Alzheimer's amyloid precursor protein.";

RL J. Neurochem. 72:549-556(1999).

RN [8]

RP INTERACTION WITH GNAO1, AND MUTAGENESIS OF 732-HIS-HIS-733.

RX MEDLINE=99162676; PubMed=10024358;

RA Brouillet E., Tremblau A., Galanaud D., Volovitch M., Boulliot C.,

RA Valenza C., Prochiantz A., Allinquant B.;

RT "The amyloid precursor protein interacts with Go heterotrimeric

RT protein within a cell compartment specialized in signal

RT transduction.";

RL J. Neurosci. 19:1717-1727(1999).

RN [9]

RP CHARACTERISTICS OF APPICAN, AND MUTAGENESIS OF SER-656.

RX MEDLINE=95256193; PubMed=7737970;

RA Pangalos M.N., Efthimiopoulos S., Shioi J., Robakis N.K.;

RT "The chondroitin sulfate attachment site of appican is formed by

RT splicing out exon 15 of the amyloid precursor gene.";

RL J. Biol. Chem. 270:10388-10391(1995).

RN [10]

RP BETA-AMYLOID METAL-BINDING.

RX MEDLINE=99316162; PubMed=10386999;

RA Huang X., Atwood C.S., Hartshorn M.A., Multhaup G., Goldstein L.E.,

RA Scarpa R.C., Quajungco M.P., Gray D.N., Lim J., Moir R.D., Tanzi R.E.,

RA Bush A.I.;

RT "The A beta peptide of Alzheimer's disease directly produces hydrogen

RT peroxide through metal ion reduction.";

RL Biochemistry 38:7609-7616(1999).

RN [11]

RP BETA-AMYLOID ZINC BINDING.

RX MEDLINE=99343552; PubMed=10413512;

RA Liu S.T., Howlett G., Barrow C.J.;

RT "Histidine-13 is a crucial residue in the zinc ion-induced aggregation

RT of the A beta peptide of Alzheimer's disease.";

RL Biochemistry 38:9373-9378(1999).

RN [12]

RP IMPORTANCE OF GLY-704 IN FREE RADICAL PROPAGATION, AND MUTAGENESIS OF

RP GLY-704.

RX MEDLINE=21956095; PubMed=11959460;

RA Kanski J., Varadarajan S., Akseanova M., Butterfield D.A.;

RT "Role of glycine-33 and methionine-35 in Alzheimer's amyloid beta-

RT peptide 1-42-associated oxidative stress and neurotoxicity.";

RL Biochim. Biophys. Acta 1586:190-198(2001).

RN [13]

RP PHOSPHORYLATION.

RX MEDLINE=97239592; PubMed=9085254;

RA Oishi M., Nairn A.C., Czernik A.J., Lim G.S., Ischura T., Gandy S.E.,

RA Greengard P., Suzuki T.;
 RT "The cytoplasmic domain of Alzheimer's amyloid precursor protein is
 RT phosphorylated at Thr654, Ser655, and Thr668 in adult rat brain and
 RT cultured cells."; Mol. Med. 3:111-123(1997).
 RL [14]
 RN PHOSPHORYLATION ON SER-730.
 RP MEDLINE=99262094; PubMed=10329382;
 RX Isohara T., Horuchi A., Watanabe T., Ando K., Czernik A.J., Uno I.,
 RA Greengard P., Nairn A.C., Suzuki T.;
 RA "Phosphorylation of the cytoplasmic domain of Alzheimer's beta-amyloid
 RT precursor protein at Ser655 by a novel protein kinase."; J.
 RL Biochem. Biophys. Res. Commun. 258:300-305(1999).
 RN [15]
 RP PHOSPHORYLATION, INDUCTION, SUBCELLULAR LOCATION, AND MUTAGENESIS OF
 RP THR-743.
 RX MEDLINE=99274744; PubMed=10341243;
 RX Ando K., Oishi M., Takeda S., Iijima K.-I., Isohara T.,
 RA Kirino Y., Greengard P., Suzuki T.;
 RA "Role of phosphorylation of Alzheimer's amyloid precursor protein
 RT during neuronal differentiation."; J. Neurosci. 19:4421-4427(1999).
 RL [16]
 RN PHOSPHORYLATION ON THR-743.
 RP MEDLINE=20396183; PubMed=10936190;
 RX Iijima K.-I., Ando K., Takeda S., Satoh Y., Seki T., Itchaha S.,
 RA Greengard P., Kirino Y., Nairn A.C., Suzuki T.;
 RA "Neuron-specific phosphorylation of Alzheimer's beta-amyloid precursor
 RT protein by cyclin-dependent kinase 5."; J. Neurochem. 75:1085-1091(2000).
 RL [17]
 RN CARBOHYDRATE STRUCTURE OF APPICAN.
 RP MEDLINE=21463085; PubMed=11479316;
 RX Tsuchida K., Shioi J., Yamada S., Boghosian G., Wu A., Cai H.,
 RA Sugahara K., Robakis N.K.;
 RA "Appican, the proteoglycan form of the amyloid precursor protein,
 RT contains chondroitin sulfate E in the repeating disaccharide region
 RL and 4-O-sulfated galactose in the linkage region."; J. Biol. Chem. 276:37155-37160(2001).
 CC -!- FUNCTION: Functions as a cell surface receptor and performs
 CC physiological functions on the surface of neurons relevant to
 CC neurite growth, neuronal adhesion and axonogenesis. Involved in
 CC cell motility and transcription regulation through protein-protein
 CC interactions (By similarity). Can promote transcription activation
 CC through binding to APBB1/Tip60 and inhibit Notch signaling through
 CC interaction with Numb (By similarity). Couples to apoptosis-
 CC inducing pathways such as those mediated by G(O) and JIP. Inhibits
 CC G(O) alpha ATPase activity. Acts as a kinesin I membrane receptor,
 CC mediating the axonal transport of beta-secretase and presenilin 1
 CC (By similarity). May be involved in copper homeostasis/oxidative
 CC stress through copper ion reduction. Can regulate neurite
 CC outgrowth through binding to components of the extracellular
 CC matrix such as heparin and collagen I and IV (By similarity). The
 CC splice isoforms that contain the BPTI domain possess protease
 CC inhibitor activity (By similarity).
 CC -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
 CC with metal-reducing activity. Bind transient metals such as

CC copper, zinc and iron. Rat and mouse beta-amyloid peptides bind
 CC only weakly transient metals and have little reducing activity due
 CC to substitutions of transient metal chelating residues. Beta-APP42
 CC may activate mononuclear phagocytes in the brain and elicit
 CC inflammatory responses. Promotes both tau aggregation and tau
 CC mediated phosphorylation (By similarity).
 CC -!- FUNCTION: Appicans elicit adhesion of neural cells to the
 CC extracellular matrix and may regulate neurite outgrowth in the
 CC brain.
 CC -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
 CC peptides, including C31, are potent enhancers of neuronal
 CC apoptosis (By similarity).
 CC -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
 CC cytoplasmic proteins, including APBB family members, the APPA
 CC family, MAPKIP1, SHC1 and Numb and Dab1 (By similarity). Binding
 CC to Dab1 inhibits its serine phosphorylation (By similarity). Also
 CC interacts with GPCR-like protein BPP, FPHU1, APPBP1, IBI, KNS2
 CC (via its TPR domains), APPBP2 (via BASS) (By similarity) and DDB1.
 CC In vitro, it binds MAPT via the MT-binding domains (By
 CC similarity). Associates with microtubules in the presence of ATP
 CC and in a kinesin-dependent manner (By similarity). Interacts,
 CC through a C-terminal domain, with GNAO1. Amyloid beta-42 binds
 CC CHRNA7 in hippocampal neurons (By similarity). Beta-amyloid
 CC associates with HADH2 (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
 CC protein that rapidly becomes internalized via clathrin-coated
 CC pits. During maturation, the immature APP (N-glycosylated in the
 CC Query Match 100.0%; Score 62; DB 1; Length 770;
 CC Best Local Similarity 100.0%; Pred. No. 0.00062;
 CC Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KKQVTSIHGG 11
 Db 724 KKQVTSIHGG 734
 Search completed: October 4, 2004, 18:57:18
 Job time : 20.087 secs

OM protein - protein search, using sw model
Run on: October 4, 2004, 18:37:37 ; Search time 52.1304 Seconds
(without alignments)
66.577 Million cell updates/sec

Title: US-10-048-203-4
Perfect score: 62
Sequence: 1 KKKQYTSIHG 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues 1017041
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp Vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
------------	-------	-------	--------	----	-------------

RESULT 1				
ID	Q97917	PRELIMINARY:	PRT:	49 AA.
AC	Q97917			
DT	01-MAY-1999	(TREMBLrel. 10, Created)		
DT	01-MAY-1999	(TREMBLrel. 10, Last sequence update)		
DT	01-JUN-2003	(TREMBLrel. 24, Last annotation update)		

ALIGNMENTS

1	62	100.0	49	6	Q97917	Q97917 bos taurus
2	62	100.0	113	13	Q8JH58	Q8JH58 chelydra se
3	62	100.0	218	11	Q8SPV5	Q8SPV5 mus musculus
4	62	100.0	384	11	Q8BFC7	Q8BFC7 mus musculus
5	62	100.0	534	13	Q93296	Q93296 gallus gall
6	62	100.0	563	13	Q9PVL1	Q9PVL1 gallus gall
7	62	100.0	693	13	Q9DGJ8	Q9DGJ8 gallus gall
8	62	100.0	699	13	Q57394	Q57394 narke japon
9	62	100.0	751	13	Q9DGJ7	Q9DGJ7 gallus gall
10	59	95.2	239	13	Q8UUI7	Q8UUI7 brachydanio
11	59	95.2	357	13	Q8UUI8	Q8UUI8 brachydanio
12	59	95.2	472	13	Q8UUS0	Q8UUS0 brachydanio
13	59	95.2	612	13	Q919E7	Q919E7 brachydanio
14	59	95.2	678	13	Q72ZT1	Q72ZT1 brachydanio
15	59	95.2	693	13	Q98SG0	Q98SG0 xenopus lae
16	59	95.2	694	13	Q8UUR9	Q8UUR9 brachydanio
17	59	95.2	695	13	Q98SF9	Q98SF9 xenopus lae
18	59	95.2	695	13	Q72XQ0	Q72XQ0 xenopus lae
19	59	95.2	736	13	Q90W28	Q90W28 brachydanio
20	59	95.2	747	13	Q91963	Q91963 xenopus. ap
21	50	80.6	82	4	Q16020	Q16020 homo sapien
22	50	80.6	82	4	Q16014	Q16014 homo sapien
23	50	80.6	82	4	Q16019	Q16019 homo sapien
24	42	67.7	133	5	Q17443	Q17443 brevicoxyne
25	41	66.1	464	10	Q9FEP0	Q9FEP0 adonis pala
26	40	64.5	251	13	Q8AWR6	Q8AWR6 brachydanio
27	40	64.5	398	16	Q7V477	Q7V477 prochloroco
28	40	64.5	452	10	Q9SZ00	Q9SZ00 arabidopsis
29	40	64.5	466	10	Q94B35	Q94B35 arabidopsis
30	39	62.9	71	16	Q816L5	Q816L5 bacillus ce
31	39	62.9	164	16	Q81P90	Q81P90 bacillus an
32	39	62.9	578	5	Q81CK3	Q81CK3 plasmodium
33	38	61.3	228	16	Q8AOP0	Q8AOP0 bacteroides
34	38	61.3	289	16	Q8RIL2	Q8RIL2 fuschacteri
35	38	61.3	451	2	Q9RCU3	Q9RCU3 staphylococ
36	38	61.3	451	16	Q8CTZ4	Q8CTZ4 staphylococ
37	38	61.3	1495	5	Q8IKI3	Q8IKI3 plasmodium
38	37	59.7	71	16	Q83DX8	Q83DX8 coxiella bu
39	37	59.7	158	10	Q8GWR9	Q8GWR9 arabidopsis
40	37	59.7	208	11	Q8ROR7	Q8ROR7 mus musculus
41	37	59.7	210	10	Q9LSU4	Q9LSU4 arabidopsis
42	37	59.7	264	13	Q804V7	Q804V7 brachydanio
43	37	59.7	267	10	Q39092	Q39092 arabidopsis
44	37	59.7	271	13	Q8AW31	Q8AW31 brachydanio
45	37	59.7	272	13	Q8JFS9	Q8JFS9 brachydanio

Q8BPC7
ID Q8BPC7 PRELIMINARY; PRT; 384 AA.
AC Q8BPC7
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Amyloid beta (Fragment).
GN APP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=22354683; PubMed=1246881;
RA The FANTOM Consortium.
RA "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573(2002).
DR EMBL; AK076506; BAC36369.1; -.
DR MGD; MGI:88059; App.
DR GO; GO:0005515; F:protein binding; IPI.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR0203; AMYLOIDA4.
DR PROSITE; PS00320; A4_INTRA; 1.
FT NON_TER 1
SQ SEQUENCE 384 AA; 43990 MW; A81B1AD8AE683173 CRC64;
Query Match 100.0%; Score 62; DB 11; Length 384;
Best Local Similarity 100.0%; Pred. No. 0.0031;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KKQYTSIHG 11
Db 338 KKQYTSIHG 348
RESULT 5
ID Q93296 PRELIMINARY; PRT; 534 AA.
AC Q93296
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Amyloid protein (fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Coulson E.J., Palliga K., Beyreuther K., Masters C.L.;
RT "What the evolution of the amyloid protein precursor supergene family
RT tells us about its function."
RL Neurochem. Int. 0:0-0(2000).
DR EMBL; AF030341; AAF12696.1; -.
DR HSP; P05067; IBA4.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR008154; A4_extra.
DR Pfam; PF02177; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
FT NON_TER 1
SQ SEQUENCE 534 AA; 60597 MW; FB53EC2E66D4C92 CRC64;
Query Match 100.0%; Score 62; DB 13; Length 534;
Best Local Similarity 100.0%; Pred. No. 0.0044;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KKQYTSIHG 11
Db 488 KKQYTSIHG 498
RESULT 6
ID Q9PVL1 PRELIMINARY; PRT; 569 AA.
AC Q9PVL1
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Amyloid protein (fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Coulson E.J., Palliga K., Beyreuther K., Masters C.L.;
RT "What the evolution of the amyloid protein precursor supergene family
RT tells us about its function."
RL Neurochem. Int. 0:0-0(2000).
DR EMBL; AF030341; AAF12696.1; -.
DR HSP; P05067; IBA4.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR008154; A4_extra.
DR Pfam; PF02177; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
FT NON_TER 1
SQ SEQUENCE 534 AA; 60597 MW; FB53EC2E66D4C92 CRC64;

RA Barnes N.Y., Li L., Yoshikawa K., Schwartz L.M., Oppenheim R.W.,
RA Milligan C.E.;
RT "Increased production of amyloid precursor protein provides a
RT substrate for caspase-3 in dying motoneurons."
RL J. Neurosci. 18:5869-5880(1998).
DR EMBL; AF042096; AAC25052.1; -.
DR HSP; P05067; IBA4.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR008154; A4_extra.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR0203; AMYLOIDA4.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
FT NON_TER 1
SQ SEQUENCE 534 AA; 60597 MW; FB53EC2E66D4C92 CRC64;
Query Match 100.0%; Score 62; DB 13; Length 534;
Best Local Similarity 100.0%; Pred. No. 0.0044;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KKQYTSIHG 11
Db 488 KKQYTSIHG 498
RESULT 6
ID Q9PVL1 PRELIMINARY; PRT; 569 AA.
AC Q9PVL1
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Amyloid protein (fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Coulson E.J., Palliga K., Beyreuther K., Masters C.L.;
RT "What the evolution of the amyloid protein precursor supergene family
RT tells us about its function."
RL Neurochem. Int. 0:0-0(2000).
DR EMBL; AF030341; AAF12696.1; -.
DR HSP; P05067; IBA4.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR008154; A4_extra.
DR Pfam; PF02177; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
FT NON_TER 1
SQ SEQUENCE 534 AA; 60597 MW; FB53EC2E66D4C92 CRC64;

DR PRINTS; PRO0203; AMYLOIDA4.
 DR PROSITE; PS00319; A4_EXTRA; 1.
 DR PROSITE; PS00320; A4_INTRA; 1.
 FT NON_TER 1
 SQ SEQUENCE 569 AA; 64753 MW; 0AB8B8B51863A19D CRC64;
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 Best Local Similarity 100.0%; Pred. No. 0.0045;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KKQYTSIHG 11
 |||||
 Db 524 KKQYTSIHG 534

RESULT 7
 Q9DGJ8 PRELIMINARY; PRT; 695 AA.
 AC Q9DGJ8; 01-VAR-2001 (TrEMBLrel. 16, Created)
 DT 01-VAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Beta-amyloid precursor protein 695 isoform.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Sarasa M., Rodolase A., Sorribas V.;
 RT "Cloning of full-length chicken beta-amyloid precursor protein
 isoforms."
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF289218; AAG00593.1; -.
 DR HSSP; P05067; 1BA4.
 DR GO; GO:0016020; C:membrane; IEA.
 DR InterPro; IPR008155; A4_APP.
 DR InterPro; IPR008154; A4_extra.
 DR InterPro; IPR001255; Beta-APP.
 DR Pfam; PF02177; A4_EXTRA; 1.
 DR Pfam; PF03454; Beta-APP; 1.
 DR PRINTS; PRO0203; AMYLOIDA4.
 DR SMART; SMO0006; A4_EXTRA; 1.
 DR PROSITE; PS00319; A4_EXTRA; 1.
 DR PROSITE; PS00320; A4_INTRA; 1.
 SQ SEQUENCE 695 AA; 78565 MW; F201ED02AEC86D95 CRC64;
 Query Match 100.0%; Score 62; DB 13; Length 695;
 Best Local Similarity 100.0%; Pred. No. 0.0057;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KKQYTSIHG 11
 |||||
 Db 649 KKQYTSIHG 659

RESULT 8
 OS7394 PRELIMINARY; PRT; 699 AA.
 AC OS7394; 01-JUN-1998 (TrEMBLrel. 06, Created)
 DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE EL amyloid precursor protein 699.
 GN EL APP699.
 OS Narke japonica (Electric ray).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
 OC Elasmobranchii; Squalia; Hymnosqualia; Pristigaster; Batoidae;
 OC Torpediniformes; Narcinoidae; Naridae; Narke.
 OX NCBI_TaxID=62965;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Electric lobe;
 RX MEDLINE=98129705; PubMed=9461486;
 RA Iijima K., Lee D.-S., Okutsu J., Tomita S., Hirashima N., Kirino Y.,
 RA Suzuki T.;
 RT "cDNA isolation of Alzheimer's amyloid precursor protein from
 cholinergic nerve terminals of the electric organ of the electric
 ray."
 RL Biochem. J. 330:29-33(1998).
 DR EMBL; AB005344; BAA24230.1; -.
 DR HSSP; P05067; 1H23.
 DR GO; GO:0016020; C:membrane; IEA.
 DR InterPro; IPR008155; A4_APP.
 DR InterPro; IPR008154; A4_extra.
 DR InterPro; IPR001255; Beta-APP.
 DR Pfam; PF02177; A4_EXTRA; 1.
 DR Pfam; PF03454; Beta-APP; 1.
 DR PRINTS; PRO0203; AMYLOIDA4.
 DR SMART; SMO0006; A4_EXTRA; 1.
 DR PROSITE; PS00319; A4_EXTRA; 1.
 DR PROSITE; PS00320; A4_INTRA; 1.
 SQ SEQUENCE 699 AA; 78579 MW; 952915C309D50E5C CRC64;
 Query Match 100.0%; Score 62; DB 13; Length 699;
 Best Local Similarity 100.0%; Pred. No. 0.0057;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KKQYTSIHG 11
 |||||
 Db 653 KKQYTSIHG 663

RESULT 9
 Q9DGJ7 PRELIMINARY; PRT; 751 AA.
 AC Q9DGJ7; 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Beta-amyloid precursor protein 751 isoform.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Sarasa M., Rodolcse A., Sortibas V.;
 RT "Cloning of full-length chicken beta-amyloid precursor protein
 RT isoforms."
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF289219; AAC00594.1; -;
 DR HSSP; P05067; 1BA4.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0004867; F:serine protease inhibitor activity; IEA.
 DR InterPro; IPR008155; A4_APP.
 DR InterPro; IPR008154; A4_extra.
 DR InterPro; IPR001255; Beta_APP.
 DR InterPro; IPR002223; Kunitz_BPTI.
 DR Pfam; PF02177; A4_EXTRA; 1.
 DR Pfam; PF03494; Beta_APP; 1.
 DR Pfam; PF00014; Kunitz_BPTI; 1.
 DR PRINTS; PR00203; ANYLQIDA4.
 DR PRINTS; PR00759; BASICPTASE.
 DR ProDom; PD000222; Kunitz_BPTI; 1.
 DR SMART; SMO0006; A4_EXTRA; 1.
 DR SMART; SMO0131; KU; 1.
 DR PROSITE; PS00319; A4_EXTRA; 1.
 DR PROSITE; PS00320; A4_INTRA; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
 KW Protease inhibitor; Serine protease inhibitor.
 SQ SEQUENCE 751 AA; 84705 NW; E78E9413A803D84 CRC64;

 Query Match 100.0%; Score 62; DB 13; Length 751;
 Best local Similarity 100.0%; Pred.No. 0.0061;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 1 KKKQYTSIHG 11
 Db 705 KKKQYTSIHG 715

 Search completed: October 4, 2004, 18:56:24
 Job time : 54.1304 secs

OM protein - protein search, using sw model

Run on: October 4, 2004, 18:37:13 ; Search time 92.8696 Seconds
(without alignments)
48.679 Million cell updates/sec

Title: US-10-048-209-5

Perfect score: 92

Sequence: 1 KQIKWIFQRRMKWK 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_28Jan04:*

1: geneseqp1980s:*

2: geneseqp1990s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003as:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	92	100.0	16	4	AAB67795 Amino aci
2	89	96.7	16	2	AAM45974 Cysteine
3	89	96.7	16	2	AAW33407 Peptide 4
4	89	96.7	16	2	AAW33410 D-form pe
5	89	96.7	16	2	AAW2958 Oestrogen
6	89	96.7	16	2	AAW56397 Preferred
7	89	96.7	16	2	AAW71270 Antennape
8	89	96.7	16	2	AAW71316 Antennape
9	89	96.7	16	2	AAW30508 Drosophil

10	89	96.7	16	2	AAW91046 Internali
11	89	96.7	16	2	AAW52102 Peptide f
12	89	96.7	16	2	AAW00859 Peptide p
13	89	96.7	16	2	AAW13509 Signal se
14	89	96.7	16	3	AAW87920 Drosophil
15	89	96.7	16	3	AAW27060 Beta-cate
16	89	96.7	16	3	AAW93667 Peptide w
17	89	96.7	16	3	AAW67966 Carboxyfl
18	89	96.7	16	3	AAW93551 Amino aci
19	89	96.7	16	3	AAW55818 Signal se
20	89	96.7	16	3	AAW71008 Drosophil
21	89	96.7	16	3	AAW51212 Antennape
22	89	96.7	16	3	AAW51167 Drosophil
23	89	96.7	16	3	AAW10343 Peptide A
24	89	96.7	16	3	AAW19251 Fragment
25	89	96.7	16	3	AAW93178 Protegrin
26	89	96.7	16	3	AAW35694 Peptide a
27	89	96.7	16	3	AAW22023 Membrane
28	89	96.7	16	3	AAW29423 ANTP pept
29	89	96.7	16	3	AAW03927 Internali
30	89	96.7	16	3	AAW93954 Peptide u
31	89	96.7	16	3	AAW29574 Antennape
32	89	96.7	16	3	AAW14785 Carrier m
33	89	96.7	16	3	AAW14761 Drosophil
34	89	96.7	16	4	AAW73091 Rheumatol
35	89	96.7	16	4	AAW60004 Internali
36	89	96.7	16	4	AAW70753 Cell memb
37	89	96.7	16	4	AAW02974 Protein t
38	89	96.7	16	4	AAW60671 Antennape
39	89	96.7	16	4	AAW06064 Drosophil
40	89	96.7	16	4	AAW45914 HIF-1alph
41	89	96.7	16	4	AAW66996 Antennape
42	89	96.7	16	4	AAW00813 Fruit fly
43	89	96.7	16	4	AAW12205 Membrane
44	89	96.7	16	5	ABW78030 Peptide d
45	89	96.7	16	5	ABW78985 Cell pene

ALIGNMENTS

RESULT 1

AAW67795

ID AAB67795 standard; peptide; 16 AA.

XX

XC AAB67795;

XX

DT 11-JUN-2001 (first entry)

XX

DE Amino acid sequence of an internalisation peptide.

XX

KW Amyloid protein precursor; APP; apoptosis; cancer; Alzheimer's disease.

XX

OS Homo sapiens.

XX

PN WO200109170-A1.

XX

PD 08-FEB-2001.
 XX
 PF 28-JUL-2000; 2000WO-FR002174.
 XX
 PR 30-JUL-1999; 99FR-00009929.
 XX
 PA (CNRS) CNRS CENT NAT RECH SCI.
 XX
 PI Allinquant B, Prochiantz A;
 XX
 DR WPI; 2001-257398/26.
 XX
 PT Peptides derived from the cytoplasmic domain of the amyloid protein
 PT precursor, useful in the treatment of cancer and Alzheimer's disease.
 PT
 PS Claim 3; Page 13; 28pp; French.
 XX
 CC The present sequence represents an internalisation peptide. It may be
 CC attached to peptides derived from the cytoplasmic domain of the human
 CC amyloid protein precursor (APP). APP peptides derived from the
 CC cytoplasmic domain, and containing the membrane domain juxtaposed to the
 CC cytoplasmic domain of APP are useful for selecting and screening products
 CC capable of inhibiting apoptosis. The peptides are useful in the treatment
 CC of cancer and Alzheimer's disease
 XX
 SQ Sequence 16 AA;
 Query Match 100.0%; Score 92; DB 4; Length 16;
 Best Local Similarity 100.0%; Pred. No. 1e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KQIKWFOQRNRMKWK 16
 Db 1 KQIKWFOQRNRMKWK 16
 RESULT 2
 AAW45974
 ID AAW45974 standard; peptide; 16 AA.
 XX
 AC AAW45974;
 XX
 DT 01-JUL-1998 (first entry)
 XX
 DE Cysteine protease inhibiting peptide for preventing cell death.
 XX
 KW Neuronal cell death; neurodegenerative disorder; inhibition;
 KW cysteine protease; cardiovascular; liver disease.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1
 FT /note= "N-3-nitro-2-pyridyl-sulphenyl-Arg"
 XX
 PN W09735876-Al.
 XX

PD 02-OCT-1997.
 XX
 PF 04-MAR-1997; 97WO-US004159.
 XX
 PR 04-MAR-1996; 96US-00610220.
 XX
 PA (UNCO) UNIV COLUMBIA NEW YORK.
 XX
 PI Troy CM;
 XX
 DR WPI; 1997-499561/45.
 XX
 PT New cysteine protease inhibiting peptide(s) for preventing cell death -
 PT in cases of neurodegenerative, cardiovascular and liver diseases, and
 PT their peptidomimetics, and general method for identifying enzyme
 PT inhibiting peptides.
 XX
 PS Claim 6; Page 68; 112pp; English.
 XX
 CC This sequence represents a specifically claimed peptide of the formula: V
 CC -(AA1)n-Cys(V')-(AA2)m-V' (I), in which n and m = 0-5, totalling 2-5; if
 CC n = 1, AA1 = Ala; if n = 2, (AA1)n = Gln-Ala; and if n = 3 or more, (AA1)n
 CC = (X)p-Gln-Ala; X = any amino acid; p = 1-3, depending on value of n; if
 CC m = 1, AA2 = Arg; if m = 2, (AA2)n = Arg-Gly; if m = 3 or more, (AA2)n =
 CC Arg-Gly-(X)q; q = 1-3, depending on value of m; V, V' and V'', any or all
 CC of which may be absent, = agent able to direct the compound to a specific
 CC cell. The peptides are inhibitors of cysteine proteases, specifically
 CC of Interleukin-1 beta converting enzyme (ICE). They inhibit death of cells,
 CC particularly in humans, and can be used to treat neurodegenerative
 CC diseases (e.g. ageing, Alzheimer's, Machado-Joseph, Parkinson's or
 CC Huntington's diseases, multiple sclerosis, muscular dystrophy, stroke),
 CC cardiovascular disease and liver disorders. The peptides should be more
 CC specific than pseudosubstrate inhibitors
 XX
 SQ Sequence 16 AA;
 Query Match 96.7%; Score 89; DB 2; Length 16;
 Best Local Similarity 93.8%; Pred. No. 2.7e-06;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KQIKWFOQRNRMKWK 16
 Db 1 KQIKWFOQRNRMKWK 16
 RESULT 3
 AAW33407
 ID AAW33407 standard; peptide; 16 AA.
 XX
 AC AAW33407;
 XX
 DT 27-AUG-2003 (revised)
 DT 17-MAR-1998 (first entry)
 XX
 DE Peptide 43-58 of homeodomain Antp.
 XX
 KW homeodomain; transcription factor; Antennapedia; Antp; vector;

transfection; hydrophobic.
 Unidentified.
 WO9712912-A1.
 10-APR-1997.
 04-OCT-1996; 96WO-FR001553.
 05-OCT-1995; 95FR-00011714.
 (CNRS) CNRS CENT NAT RECH SCI.
 Chassaing G, Prochiantz A;
 WPI; 1997-226166/20.
 New peptide(s) of high hydrophobic amino acid content - useful as vectors for delivering peptides and nucleic acids to cells.
 Claim 1; Page 7; 35pp; French.
 New peptides are provided which are 16 amino acids long and which are analogues of the peptide corresponding to residues 43-58 of the Antennapedia transcription factor homeodomain (AntpHD). The peptides contain 6-10 hydrophobic amino acids. They have the general formula: X1-X2-X3-X4-X5-Trp-X7-X8-X9-X10-X11-X12-X13-X14-X15-X16 or X16-X15-X14-X13-X12-X11-X10-X9-X8-X7-Trp-X5-X4-X3-X2-X1 in which X1-X5 and X7-X16 are any alpha-amino acids, provided that: (1) the peptide contains 6-10 hydrophobic amino acids; (2) X3 and X5 are not both Val; and (3) the natural Antp 43-58 sequence RQIKWQNRRMKWKK (i.e. the present sequence) is excluded. Specific examples of these peptides are given in AAW33408 - AAW33416. The peptides are used as vectors for introducing into live cells compounds which affect cell function, esp. peptides and nucleic acids. They can cross cellular membranes and reach various cell compartments. They are as effective as helix 3 of a homeodomain peptide. (Updated on 27-AUG-2003 to correct OS field.)
 Sequence 16 AA;
 Query Match 96.7%; Score 89; DB 2; Length 16;
 Best Local Similarity 93.8%; Pred. No. 2.7e-06;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RQIKWQNRRMKWKK 16
 :|||||
 Db 1 RQIKWQNRRMKWKK 16
 RESULT 4
 AAW33410
 ID AAW33410 standard; peptide; 16 AA.
 XX
 AC AAW33410;
 XX
 DT 17-MAR-1998 (first entry)

XX DE D-form peptide 43-58 of homeodomain Antp.
 XX homeodomain; transcription factor; Antennapedia; Antp; vector;
 KW transfection; hydrophobic.
 XX OS Synthetic.
 XX Key Location/Qualifiers
 FH Misc-difference 1..16
 FT /note= "all residues are D-form"
 FT Modified-site 1
 FT /note= "in determining the ability of this sequence to be internalised in cells, a biotin-aminopentanoyl group was attached to the N-terminal"
 FT
 XX WO9712912-A1.
 PN
 PD 10-APR-1997.
 XX
 PF 04-OCT-1996; 96WO-FR001553.
 XX
 PR 05-OCT-1995; 95FR-00011714.
 XX
 PA (CNRS) CNRS CENT NAT RECH SCI.
 PI Chassaing G, Prochiantz A;
 XX WPI; 1997-226166/20.
 XX
 PT New peptide(s) of high hydrophobic amino acid content - useful as vectors for delivering peptides and nucleic acids to cells.
 XX
 PS Disclosure; Page 7; 35pp; French.
 XX
 CC New peptides are provided which are 16 amino acids long and which are analogues of the peptide corresponding to residues 43-58 of the Antennapedia transcription factor homeodomain (AntpHD). The peptides contain 6-10 hydrophobic amino acids. They have the general formula: X1-X2-X3-X4-X5-Trp-X7-X8-X9-X10-X11-X12-X13-X14-X15-X16 or X16-X15-X14-X13-X12-X11-X10-X9-X8-X7-Trp-X5-X4-X3-X2-X1 in which X1-X5 and X7-X16 are any alpha-amino acids, provided that: (1) the peptide contains 6-10 hydrophobic amino acids; (2) X3 and X5 are not both Val; and (3) the natural Antp 43-58 sequence RQIKWQNRRMKWKK (see AAW33407) is excluded. The present sequence (the D-form of the 43-58 peptide) is a specific example of the new peptides. The peptides are used as vectors for introducing into live cells compounds which affect cell function, especially peptides and nucleic acids. They can cross cellular membranes and reach various cell compartments. They are as effective as helix 3 of a homeodomain peptide
 XX
 SQ Sequence 16 AA;
 Query Match 96.7%; Score 89; DB 2; Length 16;
 Best Local Similarity 93.8%; Pred. No. 2.7e-06;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RQIKWQNRRMKWKK 16
 :|||||
 Db 1 RQIKWQNRRMKWKK 16
 RESULT 4
 AAW33410
 ID AAW33410 standard; peptide; 16 AA.
 XX
 AC AAW33410;
 XX
 DT 17-MAR-1998 (first entry)

Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KOIKIWFQNRMRKWK 16
:|||||
Db 1 RQIKIWFQNRMRKWK 16

RESULT 6

AAW56397

ID AAW56397 standard; peptide; 16 AA.

XX

AC AAW56397;

XX

DT 05-AUG-1998 (first entry)

XX

DE Preferred signal sequence of the invention.

XX

DE Signal peptide; nuclear localisation signal; NLS;

KW immunosuppressive activity; inhibition; nuclear translocation inhibitor;

KW nuclear translocation; treatment; immune disorder; autoimmune disease;

KW hypersensitivity; sepsis; prevention; septic shock; antiviral agent;

KW tumour growth suppressor.

XX

OS Unidentified.

XX

PN WO9811907-A1.

XX

PD 26-MAR-1998.

XX

PF 15-SEP-1997; 97WO-US016217.

XX

PR 20-SEP-1996; 96US-0026978P.

PR 12-SEP-1997; 97US-00928958.

XX

PA (BRIM) BRISTOL-MYERS SQUIBB CO.

XX

PI Nadler SG, Cleaveland JS, Blake J, Haffar OK;

XX

DR WPI; 1998-217028/19.

XX

PT Nuclear translocation inhibitor polypeptides - comprising signal sequence for delivery through the cytoplasmic membrane and at least 2 nuclear localisation sequences.

XX

PS Claim 5; Page 43; 69pp; English.

XX

CC Peptides AAW56397-99 represent preferred signal sequences of the invention. They are used to construct the nuclear translocation inhibitor polypeptides of the invention. Nuclear translocation inhibitor polypeptides comprise a signal sequence peptide capable of delivering the polypeptide through the cytoplasmic membrane into a cell, and at least 2 nuclear localisation signals (NLSs). The polypeptides can be used to inhibit nuclear translocation of a cellular protein. In addition, since the nuclear translocation of certain cellular peptides is required for the host organism to mount an immune response, the polypeptide inhibitors are useful as immunosuppression agents. The polypeptides can therefore be used for the treatment of immune disorders including autoimmune diseases.

Qy 1 KOIKIWFQNRMRKWK 16
:|||||
Db 1 RQIKIWFQNRMRKWK 16

RESULT 5

AAW82958

ID AAW82958 standard; peptide; 16 AA.

XX

AC AAW82958;

XX

DT 04-FEB-1999 (first entry)

XX

DE Oestrogen receptor activity inhibiting peptide #14.

XX

XX Human; oestrogen receptor activity inhibitor; anti-oestrogen; diagnosis;

KW breast cancer; estrogen; tumour; phosphotyrosyl peptide;

KW malonyltyrosyl peptide; steroid receptor co-activator-1.

XX

OS Synthetic.

OS Homo sapiens.

XX

PN WO9846250-A1.

XX

PD 22-OCT-1998.

XX

PF 14-APR-1998; 98WO-US007711.

XX

PR 14-APR-1997; 97US-0043545P.

XX

PA (REGC) UNIV CALIFORNIA.

XX

PI Pietras RJ;

XX

DR WPI; 1998-594522/50.

XX

PI New anti-oestrogen peptide compositions - comprise sequences based on oestrogen receptor and steroid receptor co-activator-1 sequences, used for treating cancers.

XX

PS Claim 59; Page 156; 182pp; English.

XX

CC The present invention describes a composition comprising an isolated oestrogen receptor activity inhibiting (anti-oestrogen) peptide. The peptides used in the composition comprise sequences of human oestrogen receptor (OR) surrounding Tyr537 and steroid receptor co-activator-1 (SRC-1). The peptide compositions, nucleic acids and vectors of the present invention can reduce OR activity in a cell, reduced OR polypeptide dimerisation in a cell and reduce the binding of SRC-1 polypeptide to an OR polypeptide dimer in a cell. They can be used for killing cancer cells and treating cancers, particularly breast cancer. The present sequence represents a specifically claimed anti-oestrogen peptide

XX

SQ Sequence 16 AA;

Query Match 96.7%; Score 89; DB 2; Length 16;
Best Local Similarity 93.8%; Pred. No. 2.7e-06;

FD 302-100.

inhibit neurodegenerative disorder associated with e.g. ageing, Alzheimer's, Huntington's or Parkinson's disease.

XX 03-MAR-1998; 98WO-US004128.
XX 03-MAR-1997; 97US-00810540.
XX (UYCO) UNIV COLUMBIA NEW YORK.
XX Troy CM, Shelanski ML;
XX WPI; 1998-306333/43.
XX Anti-sense oligonucleotide(s) to cysteine aspartase genes - used to
XX inhibit neurodegenerative disorder associated with e.g. ageing,
XX Alzheimer's, Huntington's or Parkinson's disease.
XX Disclosure; Page 14; 60pp; English.
XX AAW71270 and AAW71315-16 represent antennapedia peptides which are used
XX to direct the antisense oligonucleotides (AAV54973-74) of the invention
XX to a cell. The antisense oligonucleotides are used to inhibit cell death
XX mediated by withdrawal of a trophic factor. AAV54973 inhibits the
XX expression of a Nedd2 rodent gene, while AAV54974 inhibits expression of
XX a human Ich-11 gene. The oligonucleotides are used to inhibit neuronal
XX cell death, especially for treatment of neuronal cell death caused by
XX e.g. aging, amyotrophic lateral sclerosis, Alzheimer's disease, Machado-
XX dentatorubral and pallidolysial atrophy, Huntington's disease, Parkinson's
XX Joseph disease, multiple sclerosis, muscular dystrophy, Parkinson's
XX disease, senility, spinocerebellar ataxia type I, spinobulbar muscular
XX atrophy, stroke or trauma
XX Sequence 16 AA;
SQ Query Match 96.7%; Score 89; DB 2; Length 16;
Best Local Similarity 93.8%; Pred. No. 2.7e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KQIKIWFQNRMRKWKX 16
:|||||
Db 1 RQIKIWFQNRMRKWKX 16
:|||||
RESULT 9
AAW30508
ID AAW30508 standard; peptide; 16 AA.
XX AAW30508;
XX 26-OCT-1998 (first entry)
XX Drosophila membrane translocation sequence.
XX DP-1; transcription factor; antagonist; E2F protein; apoptosis;
XX cell proliferation; cardiovascular cell; restenosis; tumour;
XX surgical stent; therapy; membrane translocation; antennapedia protein.
XX Drosophila melanogaster.
XX

PN WO9828334-A1.
XX 02-JUL-1998.
XX 22-DEC-1997; 97WO-GB003506.
XX 20-DEC-1996; 96GB-00026589.
XX (PROL-) PROLIFIX LTD.
XX La Thangue NB, Bandara LR;
XX WPI; 1998-377596/32.
XX Polypeptide fragments of the Dp-1 transcription factor - used for
XX inducing apoptosis, specifically in tumour and cardiovascular cells, e.g.
XX for preventing re-stenosis.
XX Disclosure; Page 5; 55pp; English.
XX This polypeptide comprises a membrane translocation sequence derived from
XX the Drosophila melanogaster antennapedia protein. Such membrane
XX translocation sequences are useful in directing entry of a polypeptide
XX into a cell. Polypeptides of the invention (see AAW30504-07) are derived
XX from the DEF box region (see AAW30501) of transcription factor Dp1. They
XX act as antagonists of the heterodimerisation of a DP protein with an E2F
XX protein, and can be used to induce apoptosis, specifically in tumour and
XX cardiovascular cells, e.g. for preventing restenosis. A claimed fusion
XX protein comprises a DEF box peptide and the Drosophila antennapedia
XX protein membrane translocation sequence
XX Sequence 16 AA;
SQ Query Match 96.7%; Score 89; DB 2; Length 16;
Best Local Similarity 93.8%; Pred. No. 2.7e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KQIKIWFQNRMRKWKX 16
:|||||
Db 1 RQIKIWFQNRMRKWKX 16
:|||||
RESULT 10
AAW91046
ID AAW91046 standard; peptide; 16 AA.
XX AAW91046;
XX 24-MAR-1999 (first entry)
XX Internalization sequence associated with cadherin modulating agents.
XX Alpha-catenin; beta-catenin; interaction; modulation; cell adhesion;
XX cadherin-mediated function; demyelinating neurological disease;
XX multiple sclerosis; drug delivery; cancer; angiogenesis; immune system;
XX central nervous system; apoptosis induction; cadherin-expression cell;
XX pregnancy prevention; vasopermeability; synaptic stability; diabetes;
XX

KW Rheumatoid arthritis; allergic response; learning; antennapedia protein;
KW antibody-mediated graft rejection; internalization sequence; memory.
XX
OS Synthetic.
XX
XX W09845319-A2.
XX
XX 15-OCT-1998.
XX
XX 14-APR-1998; 98WO-CA000322.
XX
XX 10-APR-1997; 97US-0043361P.
XX
XX (UWMC-) UNIV MCGILL.
XX
XX Blaschuk OW, Gour BJ;
XX
XX WPI; 1999-024009/02.
XX
XX New catenin modulating agents - comprising peptides having a sequence HAV
PT or analogues or antibodies, used for modulating cadherin-mediated
PT functions.
XX
XX Claim 16; Page 78; 106pp; English.
XX
XX The present sequence represents antennapedia protein derived
CC internalization sequence associated with cadherin modulating agents.
CC These agents are used for modulating cadherin-mediated functions. They
CC can be used for disrupting interaction between alpha-catenin and beta-
CC catenin in a cell; inhibiting cell adhesion, e.g. between epithelial
CC cells, endothelial cells, neural cells, tumour cells and lymphocytes, for
CC treating a demyelinating neurological disease, e.g. multiple sclerosis,
CC for reducing unwanted cellular adhesion in a mammal, for enhancing the
CC delivery of a drug through the skin of a mammal, for enhancing the
CC delivery of a drug to a tumour in a mammal, for treating cancer in a
CC mammal, for inhibiting angiogenesis in a mammal, for enhancing drug
CC delivery to the central nervous system of a mammal, for inducing
CC apoptosis in a cadherin-expression cell, for modulating the immune system
CC of a mammal, for preventing pregnancy in a mammal, for increasing
CC vasopermeability in a mammal, or for inhibiting synaptic stability in a
CC mammal. In particular they can be used for treating diabetes, rheumatoid
CC arthritis, allergic responses, antibody-mediated graft rejection or for
CC stimulating learning and memory
XX
XX Sequence 16 AA;

Query Match 96.7%; Score 89; DB 2; Length 16;
Best Local Similarity 93.8%; Pred. No. 2.7e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KQIKTFQNRMRKWK 16
:|||||
Db 1 RQIKTFQNRMRKWK 16

RESULT 11
AAV52102

ID AAV52102 standard; peptide; 16 AA.
XX
AC AAV52102;
XX
DT 28-JAN-2000 (first entry)
XX
DE Peptide from the third helix of antennapedia homeodomain protein.
XX
XX Rho binding region; Rho binding protein; ROCK II; ROCK I; Kinectin;
KW ROCK/Kinectin homology domain; cell growth; assay; Skn 7; modulator;
KW antifungal agent; antennapedia homeodomain protein; translocate.
XX
XX Drosophila melanogaster.
OS
XX W09952941-A2.
XX
XX 21-OCT-1999.
XX
XX 09-APR-1999; 99WO-GB001096.
XX
XX 09-APR-1998; 98GB-00007848.
XX
XX (MEDI-) MEDICAL RES COUNCIL.
PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY.
XX
XX Johnston LH, Treisman RH;
XX
XX WPI; 1998-620374/53.
XX
XX Assay for modulators of binding of Rho protein with its binding partners,
PT potentially useful as antifungal agents.
XX
XX Disclosure; Page 16; 66pp; English.
XX
XX This sequence is a peptide from the third helix of the Drosophila
CC antennapedia protein that translocates across biological membranes. This
CC sequence can be linked to the Rho binding region of the invention
CC (AAV52100) to cause translocation across eukaryotic cell membranes. The
CC Rho binding region is present in many Rho binding proteins, such as ROCK-
CC I, ROCK-II and Kinectin and is also referred to as the ROCK/Kinectin
CC homology domain. Rho-A is involved in many cellular processes including
CC stress fibre formation, cell motility, cytokinesis and apoptosis. The Rho
CC binding domain is used in the invention which relates to an assay for
CC potential modulators of cell growth. The assay consists of a Skn7
CC polypeptide, a beta2 polypeptide or a polypeptide consisting of a
CC ROCK/Kinectin homology domain, a Rho polypeptide which binds to the
CC previous peptide and a test compound. The modulation of the binding of
CC the two peptides caused by the test compound is measured. The method is
CC used to identify modulators, particularly antagonists, of the interaction
CC of Rho with its binding partners, e.g. to render pathogens sensitive to
CC the host's defence system, particularly as antifungal agents. The
CC ROCK/Kinectin homology domain can be used to screen databases for other
CC Rho-binding proteins
XX
XX Sequence 16 AA;

Query Match 96.7%; Score 89; DB 2; Length 16;

Best Local Similarity 93.8%; Pred. No. 2.7e-06; Mismatches 0; Indels 0; Gaps 0;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQIKWIFQNRRMKWK 16
 :|||||
 Db 1 RQIKWIFQNRRMKWK 16

RESULT 12
 AAY00859
 ID AAY00859 standard; peptide; 16 AA.
 XX AC AAY00859;
 XX DT 20-MAY-1999 (first entry)
 XX DE Peptide pAntp(43-58) used in membrane-permeable construct.
 XX KW Membrane-permeable construct; lipid membrane; membrane transport;
 KW oligonucleotide delivery; cancer therapy; signal transduction; inhibitor;
 KW gene therapy; transcription; translation; expression; replication.
 XX OS Synthetic.
 XX FH Key Location/Qualifiers
 FT Modified-site 16
 FT /note= "amidated"
 XX PN W09905302-A1.
 XX PD 04-FEB-1999.
 XX PF 16-JUL-1998; 96WO-US014761.
 XX PR 24-JUL-1997; 97US-0053678P.
 XX PA (PEKE) PERKIN-ELMER CORP.
 XX PI Langel U, Bartfai T, Pooga M, Valkna A, Saar K, Halibrink M;
 XX WPI; 1999-142952/12.
 XX PT New membrane-permeable constructs - comprise a peptide linked by a labile
 PT bond to a nucleic acid analogue capable of hybridising with an
 PT intracellular polynucleotide.
 XX PS Disclosure; Page 26; 60pp; English.
 XX CC This sequence represents a peptide used in the construct of the
 CC invention. The construct is a membrane-permeable construct for transport
 CC across a lipid membrane, which comprises: (a) a nucleic acid analogue
 CC capable of hybridising with an intracellular polynucleotide (PN); (b) a
 CC peptide; and (c) a labile bond linking the nucleic acid analogue and the
 CC peptide. The membrane-permeable constructs can be used for delivery of
 CC oligonucleotides, nucleic acids and nucleic acid analogues into cells.
 CC They can be used for e.g. cancer therapy, signal transduction studies,
 CC identifying new intracellular drug targets or gene therapy. They can also

CC be used for selectively inhibiting DNA transcription, RNA translation,
 CC RNA or DNA expression, DNA replication, or an DNA or RNA regulatory
 CC function of preselected DNA or RNA sequences in a living cell

XX SQ Sequence 16 AA;
 Query Match 96.7%; Score 89; DB 2; Length 16;
 Best Local Similarity 93.8%; Pred. No. 2.7e-06;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQIKWIFQNRRMKWK 16
 :|||||
 Db 1 RQIKWIFQNRRMKWK 16

RESULT 13
 AAY13509
 ID AAY13509 standard; peptide; 16 AA.
 XX AC AAY13509;
 XX DT 30-JUL-1999 (first entry)
 XX DE Signal sequence of antennapedia.
 XX KW Fusion protein; calpastatin; calpain; platelet aggregation; arthritis;
 KW hypoxia; erythrocyte sickling; sickle cell; HIV provirus; NF-kappaB;
 KW inflammation; asthma; immune response; restenosis; myocardial infarction;
 KW cancer; calpastat; antennapedia.
 XX OS Mammalia.
 XX PN W09922756-A1.
 XX PD 14-MAY-1999.
 XX PF 04-NOV-1998; 96WO-US023526.
 XX PR 04-NOV-1997; 97US-00964302.
 XX PA (NEWB-) NEW ENGLAND MEDICAL CENT HOSPITALS INC.
 XX PI Potter DA, Skolnik PR;
 XX WPI; 1999-326923/27.
 XX PT Fusion protein of signal sequence and calpastatin.
 XX PS Disclosure; Page 5; 46pp; English.
 XX CC The invention features fusion proteins that contain a calpastatin peptide
 CC and a signal sequence capable of delivering the fusion protein into a
 CC eukaryotic cell. The fusion protein is used for the inhibition of calpain
 CC in a cell. The fusion proteins are specifically used: (a) to prevent
 CC aggregation and degranulation of platelets (e.g. during storage); (b) to
 CC inhibit hypoxia-induced sickling of erythrocytes (during storage),
 CC facilitating subsequent transfusion of autologous cells for treatment of

CC sickle cell crises); and (c) to inhibit activation of human immune
CC deficiency virus provirus in infected cells (or similarly for other
CC viruses regulated by NF-kappaB). Other disclosed uses are: to treat or
CC prevent inflammation (e.g. arthritis or asthma), unwanted immune
CC responses (e.g. transplant rejection), restenosis (associated with
CC angioplasty), cancer, subarachnoid hemorrhage, vasospasm, muscular
CC dystrophy, cataracts and traumatic birth injury; to prevent spread of
CC platelets on surfaces (e.g. when applied to the surface of stents,
CC catheters etc.); to reduce coronary thrombosis in by-pass surgery and
CC angioplasty; to treat myocardial infarction, or to prevent progression of
CC infarction (myocardial or cerebral). The fusion protein has a reversible
CC inhibitory effect and enters cells easily. It allows platelets to be
CC stored cold with reduced change in shape
XX
SQ Sequence 16 AA;

Query Match 96.7%; Score 89; DB 2; Length 16;
Best Local Similarity 93.8%; Pred. No. 2.7e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQIKIWFQNRRMKWKK 16
:|||||
Db 1 RQIKIWFQNRRMKWKK 16

RESULT 14

AAV87920
ID AAV87920 standard; peptide; 16 AA.

XX AC AAV87920;
XX DT 11-SEP-2000 (first entry)
XX DE Drosophila sp. antennapedia protein fragment.

XX Rad51; cell proliferation; rad51TRI-131; rad51K-A134; immunosuppressive;
KW cytostatic; antiinflammatory; antiproliferative; programmed cell death;
KW treatment; autoimmune disorder; inflammation; cancer; graft rejection;
KW proliferative disorder; hyperproliferative disorder; antennapedia.

XX OS Drosophila sp.

XX FN US6057104-A.

XX PN 02-MAY-2000.

XX PF 05-NOV-1997; 97US-00964614.

XX PR 05-NOV-1996; 96US-00756280.

XX PA (LEXI-) LEXICON GENETICS INC.

XX PI Hasty P;

XX DR WPI; 2000-349568/30.

XX PT Mutant forms of mammalian Rad51 proteins and polypeptides that disrupt

PT cell proliferation and promote programmed cell death, encoded by specific
PT nucleotides.

XX PS Disclosure; Col 31-32; 22pp; English.

XX This invention describes novel truncated and altered forms of Rad51
CC products encoded by rad51TRI-131 and rad51K-A134. The products of the
CC invention have immunosuppressive, cytostatic, antiinflammatory and
CC antiproliferative activity. Altered and mutant forms of Rad51 are useful
CC for inhibiting cell proliferation and for promoting programmed cell
CC death. Therapeutic agents, factors or compounds capable of disrupting the
CC essential processes mediated by or associated with normal Rad51 or Rad52
CC are useful for treating diseases like autoimmune disorders, inflammation,
CC cancer, graft rejection and other proliferative and hyperproliferative
CC disorders. This sequence represents a fragment of the Drosophila
CC antennapedia protein which is described in the method of the invention
XX
SQ Sequence 16 AA;

Query Match 96.7%; Score 89; DB 3; Length 16;

Best Local Similarity 93.8%; Pred. No. 2.7e-06;

Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQIKIWFQNRRMKWKK 16
:|||||
Db 1 RQIKIWFQNRRMKWKK 16

RESULT 15

AAE27060

ID AAE27060 standard; peptide; 16 AA.

XX AC AAE27060;

XX DT 15-FEB-2001 (first entry)

XX DE Beta-catenin derived internalisation moiety SEQ ID NO: 47.

XX KW Beta-catenin; cadherin-mediated intercellular adhesion;

XX cell differentiation; modulating agent; hair loss; skin exfoliation;

XX internalisation moiety; flanking sequence; transcription; hearing loss.

XX OS Drosophila melanogaster.

XX FN WO200053632-A1.

XX PD 14-SEP-2000.

XX PF 07-MAR-2000; 2000WO-CA000222.

XX PR 09-MAR-1999; 99US-00265107.

XX PA (UYMC-) UNIV MCGILL.

XX PI Blaschuk OW, Gour BJ;

XX DR WPI; 2000-594308/56.

XX Stimulating beta-catenin mediated gene expression, cellular
 PT differentiation and hair growth, involves contacting cells with
 PT modulating agent capable of inhibiting interaction between alpha and beta
 PT catenin.
 XX
 PS Claim 8; Page 38; 77pp; English.
 XX
 CC The present invention is concerned with methods of modulating the amount
 CC of free beta-catenin in the cell, and methods of stimulating the
 CC expression of genes involved in cellular differentiation, the
 CC transfection of which is under the control of beta-catenin. The peptides
 CC given in AAB27033-B27089, AAB27284-B27300 and AAB27330-B27351 can be used
 CC as modulating agents which interrupt the interaction between alpha and
 CC beta catenin, causing increased levels of the latter and stimulating the
 CC activation of beta-catenin mediated transcription. This can be used to
 CC stimulate cell differentiation, which can then be used to promote hair
 CC growth and skin exfoliation. This latter is particularly useful in the
 CC improvement of photodamaged skin and to minimise wrinkles. The modulating
 CC peptide can also be used to reduce hearing loss resulting from inner ear
 CC disorders such as hyperacusis and tinnitus
 XX
 SQ Sequence 16 AA;
 Query Match 96.7%; Score 89; DB 3; Length 16;
 Best Local Similarity 93.8%; Pred. No. 2.7e-06;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KQIKIWFQNRNMWKK 16
 :|||||
 Db 1 RQIKIWFQNRNMWKK 16

Search completed: October 4, 2004, 18:52:48
 Job time : 103.87 secs

GenCore version 5.1.6
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 OM protein - protein search, using sw model
 Run on: October 4, 2004, 18:45:55 ; Search time 23.6522 Seconds
 (without alignments)
 65.071 Million cell updates/sec
 Title: US-10-048-209-5
 Perfect score: 92
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 Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5
 Searched: 283366 seqs, 96191526 residues
 Total number of hits satisfying chosen parameters: 283366
 Minimum DB seq length: 0
 Maximum DB seq length: 2000000000
 Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries
 Database : PIR_78:
 1: pir1:
 2: pir2:
 3: pir3:
 4: pir4:
 Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query No.	Score	Match	Length	DB ID	Description
1	89	96.7	33	2	S57235	antennapedia prote
2	89	96.7	42	2	I65241	homeotic protein H
3	89	96.7	45	2	PC1216	homeotic protein D
4	89	96.7	48	2	I51439	homeobox protein -
5	89	96.7	66	2	S15536	homeotic protein H
6	89	96.7	66	2	S15538	homeotic protein H
7	89	96.7	71	2	JC1161	homeotic protein 3
8	89	96.7	71	2	A60084	homeotic protein H
9	89	96.7	74	2	D34510	homeotic protein H
10	89	96.7	75	2	I51341	homeo box protein
11	89	96.7	75	2	S98852	homeotic protein S
12	89	96.7	76	2	C43559	homeotic protein R
13	89	96.7	78	2	I51342	homeo box protein

14 89 96.7 81 2 S47605 homeotic protein H
15 89 96.7 81 2 B2585 homeotic protein H
16 89 96.7 82 2 S08302 homeotic protein H
17 89 96.7 83 2 S47603 homeotic protein H
18 89 96.7 83 2 S50066 homeotic protein H
19 89 96.7 86 2 A34510 homeotic protein Z
20 89 96.7 86 2 J70489 homeotic protein Z
21 89 96.7 86 2 S08303 homeotic protein H
22 89 96.7 87 2 S00589 homeotic protein M
23 89 96.7 88 2 A03317 homeotic protein M
24 89 96.7 96 2 S08639 homeotic protein H
25 89 96.7 96 2 A05266 homeotic protein H
26 89 96.7 97 2 C27176 homeotic protein H
27 89 96.7 97 2 A24779 homeotic protein M
28 89 96.7 103 2 A32167 homeotic protein H
29 89 96.7 105 2 S47602 homeotic protein H
30 89 96.7 105 2 A27471 homeotic protein R
31 89 96.7 106 2 S36448 homeotic protein T
32 89 96.7 107 2 B61045 homeobox protein -
33 89 96.7 113 2 T10775 homeotic protein H
34 89 96.7 118 2 A24777 homeotic protein H
35 89 96.7 118 2 J70273 homeotic protein M
36 89 96.7 118 2 B24777 homeotic protein M
37 89 96.7 119 2 A03314 homeotic protein b
38 89 96.7 138 2 S20087 homeobox A5 protei
39 89 96.7 148 2 PC4071 homeotic protein H
40 89 96.7 153 1 WJHU3C homeotic protein H
41 89 96.7 153 1 WJMSX6 homeotic protein H
42 89 96.7 158 2 A27348 homeotic protein H
43 89 96.7 209 2 A43553 homeotic protein H
44 89 96.7 217 1 WJHU2C homeotic protein H
45 89 96.7 217 1 WJMSX2 homeotic protein H

ALIGNMENTS

RESULT 1
S57235 antennapedia protein (clone pl105) - fruit fly (Drosophila pseudoobscura)
(fragment)
C/Species: Drosophila pseudoobscura
C/Date: 10-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 15-Oct-1999
C/Accession: S57235
R/Randazzo, F.M.; Seeger, M.A.; Huss, C.A.; Sweeney, M.A.; Cecil, J.K.; Kaufman, T.C.
Genetics 133, 319-330, 1993
A/Title: Structural changes in the antennapedia complex of Drosophila pseudoobscura.
A/Reference number: S57224
A/Accession: S57235
A/Molecule type: DNA
A/Residues: 1-33 <RAN>
A/Cross-references: EMBL:X77711
C/Genetics:
A/Gene: FlyBase:Antp
A/Cross-references: FlyBase:FBgn0012693

C/Superfamily: unassigned homeobox proteins; homeobox homology
C/Keywords: DNA binding; homeobox; nucleus; transcription regulation
F/1-22/Domain: homeobox homology (fragment) <Hox>

Query Match 96.7%; Score 89; DB 2; Length 33;
Best Local Similarity 93.8%; Pred. No. 3.5e-07;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KQIKWFQNRMRKWKX 16
:|||||
Db 7 RQIKWFQNRMRKWKX 22

RESULT 2

I65241 homeotic protein Hox-A - rat (fragment)
C/Species: Rattus norvegicus (Norway rat)
C/Date: 27-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 15-Oct-1999
C/Accession: I65241
R/Sakayama, Y.; Mizuta, I.; Ogasawara, N.; Yoshikawa, H.
Biochem. Genet. 32, 351-360, 1994
A/Title: Cloning of rat homeobox genes.
A/Reference number: I52340; MUID:95217128; PMID:7702549
A/Accession: I65241
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-42 <RES>
A/Cross-references: GS:S76290; NID:g913077
C/Genetics:
A/Gene: Hox-A; Hox-1
C/Superfamily: unassigned homeobox proteins; homeobox homology
C/Keywords: DNA binding; homeobox; nucleus; transcription regulation
F/1-40/Domain: homeobox homology (fragment) <Hox>

Query Match 96.7%; Score 89; DB 2; Length 42;
Best Local Similarity 93.8%; Pred. No. 4.4e-07;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KQIKWFQNRMRKWKX 16
:|||||
Db 25 RQIKWFQNRMRKWKX 40

RESULT 3

PC1216 homeotic protein Dtdbx1 - planarian (Dugesia tigrina) (fragment)
C/Species: Dugesia tigrina
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 17-Oct-1997
C/Accession: PC1216
R/Oliver, G.; Vispo, M.; Mailhos, A.; Martinez, C.; Sosa-Pineda, B.; Fielitz, W.; Ehrlich, R.
Gene 121, 337-342, 1992
A/Title: Homeoboxes in flatworms.
A/Reference number: JCI386; MUID:93077050; PMID:1359988
A/Accession: PC1216
A/Molecule type: DNA
A/Residues: 1-45 <OLI>

A/Cross-references: EMBL:X66822
 C/Superfamily: unassigned homeobox proteins; homeobox homology
 C/Keywords: DNA binding; homeobox; nucleus; transcription regulation
 F/1-43/Domain: homeobox homology (fragment) <HOX>

Query Match 96.7%; Score 89; DB 2; Length 45;
 Best Local Similarity 93.8%; Pred. No. 4.7e-07;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KQIKWFOQNRMRKWK 16
 :|||||
 Db 30 RQIKWFOQNRMRKWK 45

RESULT 4
 151439
 homeobox protein - African clawed frog (fragment)
 C/Species: Xenopus laevis (African clawed frog)
 C/Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 15-Oct-1999
 C/Accession: 151439
 R/Leroy, P.; DeRobertis, E.M.
 Dev. Dyn. 194, 21-32, 1992
 A/Title: Effects of lithium chloride and retinoic acid on the expression of
 genes from the *Xenopus laevis* Hox 2 complex.
 A/Reference number: 151439; PMID:1384809
 A/Accession: 151439
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-48 <LER>
 A/Cross-references: GB:M91587; NID:g214257; PIDN:AAA49750.1; PID:g214258
 C/Genetics:
 A/Gene: Hox2.2
 C/Superfamily: unassigned homeobox proteins; homeobox homology
 C/Keywords: DNA binding; homeobox; nucleus; transcription regulation
 F/1-27/Domain: homeobox homology (fragment) <HOX>

Query Match 96.7%; Score 89; DB 2; Length 48;
 Best Local Similarity 93.8%; Pred. No. 5e-07;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KQIKWFOQNRMRKWK 16
 :|||||
 Db 12 RQIKWFOQNRMRKWK 27

RESULT 5
 151536
 homeotic protein Hox A7 - human (fragment)
 N/Alternate names: homeotic protein Hox 1A
 C/Species: Homo sapiens (man)
 C/Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 29-Aug-1997
 C/Accession: 151536
 R/Boncinelli, E.; Acampora, D.; Pannese, M.; d'Esposito, M.; Somma, R.; Gaudino,
 G.; Stornaiuolo, A.; Caffiero, M.; Faiella, A.; Simeone, A.
 Genome 31, 743-756, 1989
 A/Title: Organization of human class I homeobox genes.
 A/Reference number: S15036; MUID:90215256; PMID:2576652

A/Accession: S15536
 A/Status: not compared with conceptual translation
 A/Molecule type: DNA
 A/Residues: 1-66 <BON>
 C/Genetics:
 A/Gene: GDB:HOXA6
 A/Cross-references: GDB:120648; OMIM:142951
 A/Map position: 7p15.3-7p15.3
 C/Superfamily: unassigned homeobox proteins; homeobox homology
 C/Keywords: DNA binding; homeobox; nucleus; transcription regulation
 F/2-58/Domain: homeobox homology <HOX>

Query Match 96.7%; Score 89; DB 2; Length 66;
 Best Local Similarity 93.8%; Pred. No. 6.8e-07;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KQIKWFOQNRMRKWK 16
 :|||||
 Db 43 RQIKWFOQNRMRKWK 58

RESULT 7
 JCL161
 homeotic protein 3.4 - eastern newt (fragment)

A/Accession: S15536
 A/Status: not compared with conceptual translation
 A/Molecule type: DNA
 A/Residues: 1-66 <BON>
 C/Genetics:
 A/Gene: GDB:HOXA7
 A/Cross-references: GDB:120647; OMIM:142950
 A/Map position: 7p15.3-7p15.3
 C/Superfamily: unassigned homeobox proteins; homeobox homology
 C/Keywords: DNA binding; homeobox; nucleus; transcription regulation
 F/2-58/Domain: homeobox homology <HOX>

Query Match 96.7%; Score 89; DB 2; Length 66;
 Best Local Similarity 93.8%; Pred. No. 6.8e-07;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KQIKWFOQNRMRKWK 16
 :|||||
 Db 43 RQIKWFOQNRMRKWK 58

RESULT 7
 JCL161
 homeotic protein 3.4 - eastern newt (fragment)

C;Species: Notophthalmus viridescens, Triturus viridescens (eastern newt)
 C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 23-May-1997
 C;Accession: JCI1161
 R;Belleville, S.; Beauchemin, M.; Tremblay, M.; Noiseux, N.; Savard, P.
 Gene 114, 179-186, 1992
 A;Title: Homeobox-containing genes in the newt are organized in clusters similar to other vertebrates.
 A;Reference number: JCI1161; MUID:92290273; PMID:1351019
 A;Accession: JCI1161
 A;Molecule type: DNA
 A;Residues: 1-71 <BEL>
 A;Status: preliminary
 A;Cross-references: GS:M84001
 C;Genetics:
 A;Gene: NvHox-3.4
 C;Superfamily: unassigned homeobox proteins; homeobox homology
 C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
 F;5-61/Domain: homeobox homology <Hox>

Query Match 96.7%; Score 89; DB 2; Length 71;
 Best Local Similarity 93.8%; Pred. No. 7.3e-07;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KQIKIWFQNRMRMKWK 16
 :|||||
 Db 46 RQIKIWFQNRMRMKWK 61

RESULT 8
 A60084
 homeotic protein Hox 3.4 - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 20-Feb-1993 #sequence_revision 20-Feb-1993 #text_change 07-May-1999
 C;Accession: A60084
 R;Gaunt, S.J.; Coletta, P.L.; Pravtcheva, D.; Sharpe, P.T.
 Development 169, 329-339, 1990
 A;Title: Mouse Hox-3.4: homeobox sequence and embryonic expression patterns compared with other members of the Hox gene network.
 A;Reference number: A60084; MUID:90382249; PMID:1976088
 A;Accession: A60084
 A;Status: not compared with conceptual translation
 A;Molecule type: DNA
 A;Residues: 1-71 <GAU>
 C;Genetics:
 A;Map position: 15
 C;Superfamily: unassigned homeobox proteins; homeobox homology
 C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
 F;5-61/Domain: homeobox homology <Hox>

Query Match 96.7%; Score 89; DB 2; Length 71;
 Best Local Similarity 93.8%; Pred. No. 7.3e-07;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KQIKIWFQNRMRMKWK 16
 :|||||
 Db 46 RQIKIWFQNRMRMKWK 61

RESULT 9
 D34510
 homeotic protein H90 - honeybee (fragment)
 C;Species: Apis mellifera (honeybee)
 C;Date: 22-Jun-1990 #sequence_revision 09-Oct-1992 #text_change 24-Sep-1999
 C;Accession: D34510
 R;Walldorf, U.; Flaig, R.; Gehring, W.J.
 Proc. Natl. Acad. Sci. U.S.A. 86, 9971-9975, 1989
 A;Title: Comparison of homeobox-containing genes of the honeybee and Drosophila.
 A;Reference number: A34510; MUID:90099384; PMID:2574865
 A;Accession: D34510
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-74 <WAL>
 A;Cross-references: GB:M29493; NID:g155675; PID:AAA27728.1; PID:g155676
 A;Note: the authors translated the codons for residues 68-74
 C;Superfamily: unassigned homeobox proteins; homeobox homology
 C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
 F;9-65/Domain: homeobox homology <Hox>

Query Match 96.7%; Score 89; DB 2; Length 74;
 Best Local Similarity 93.8%; Pred. No. 7.6e-07;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KQIKIWFQNRMRMKWK 16
 :|||||
 Db 50 RQIKIWFQNRMRMKWK 65

RESULT 10
 I51341
 homeo box protein - Atlantic salmon (fragment)
 C;Species: Salmo salar (Atlantic salmon)
 C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 24-Sep-1999
 C;Accession: I51341
 R;Floge, A.; Nølven, A.; Eiken, H.G.
 Gene 62, 141-152, 1988
 A;Title: Molecular cloning and characterization of homeobox-containing genes from Atlantic salmon.
 A;Reference number: I51341; MUID:88226009; PMID:2897318
 A;Accession: I51341
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-75 <FJO>
 A;Cross-references: GB:M18903; NID:g213797; PID:AAA49559.1; PID:g213798
 C;Superfamily: unassigned homeobox proteins; homeobox homology
 C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
 F;2-58/Domain: homeobox homology <Hox>

Query Match 96.7%; Score 89; DB 2; Length 75;
 Best Local Similarity 93.8%; Pred. No. 7.7e-07;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KQIKIWFQNRMRMKWK 16
 :|||||
 Db 43 RQIKIWFQNRMRMKWK 58

```

Db          53 RQIKWIFQNRRMKWKX 68
:|||||
RESULT 11
S5852
homeotic protein Scr homolog - Junonia coenia (fragment)
N/Alternate names: sex combs reduced homeodomain protein
C/Species: Junonia coenia
C/Date: 19-Mar-1997 #sequence_revision 29-Aug-1997 #text_change 24-Sep-1999
C/Accession: S5852
R/Warren, R.W.; Nagy, L.; Selegue, J.; Gates, J.; Carroll, S.
Nature 372, 458-461, 1994
A/Title: Evolution of homeotic gene regulation and function in flies and
butterflies.
A/Reference number: S5850; MUID:95075456; PMID:7840822
A/Accession: S5852
A/Status: nucleic acid sequence not shown; translation not shown
A/Molecule type: mRNA
A/Residues: 1-75 <VAR>
A/Cross-references: EMBL:L42136; NID:g806495; PIDN:AAA68462.1; PID:g806496
A/Note: the nucleotide sequence was submitted to the EMBL Data Library, May 1995
C/Superfamily: unassigned homeobox proteins; homeobox homology
C/Keywords: DNA binding; homeobox; nucleus; transcription regulation
F:1-40/Domain: homeobox homology (fragment) <HOX>

Query Match          96.7%; Score 89; DB 2; Length 75;
Best Local Similarity 93.8%; Pred. No. 7.7e-07;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQIKWIFQNRRMKWKX 16
:|||||
Db 25 RQIKWIFQNRRMKWKX 40

RESULT 12
C43559
homeotic protein R3 - rat (fragment)
C/Species: Rattus norvegicus (Norway rat)
C/Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 24-Sep-1999
C/Accession: C43559
R/Falzon, M.; Chung, S.Y.
Development 103, 601-610, 1988
A/Title: The expression of rat homeobox-containing genes is developmentally
regulated and tissue specific.
A/Reference number: A43559; MUID:89231502; PMID:2907739
A/Accession: C43559
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-76 <FAL>
A/Cross-references: GB:K37567; NID:g204634; PIDN:AAA41343.1; PID:g204635
C/Superfamily: unassigned homeobox proteins; homeobox homology
C/Keywords: DNA binding; homeobox; nucleus; transcription regulation
F:20-76/Domain: homeobox homology (fragment) <HOX>

Query Match          96.7%; Score 89; DB 2; Length 76;
Best Local Similarity 93.8%; Pred. No. 7.8e-07;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQIKWIFQNRRMKWKX 16
:|||||
Db 1 RQIKWIFQNRRMKWKX 16

RESULT 13
151342
homeo box protein - Atlantic salmon (fragment)
C/Species: Salmo salar (Atlantic salmon)
C/Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 24-Sep-1999
C/Accession: 151342
R/Fjose, A.; Molven, A.; Eiken, H.G.
Gene 62, 141-152, 1988
A/Title: Molecular cloning and characterization of homeobox-containing genes
from Atlantic salmon.
A/Reference number: 151341; MUID:88226009; PMID:2897318
A/Accession: 151342
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-78 <EO>
A/Cross-references: GB:M18904; NID:g213799; PIDN:AAA49560.1; PID:g213800
C/Superfamily: unassigned homeobox proteins; homeobox homology
C/Keywords: DNA binding; homeobox; nucleus; transcription regulation
F:2-58/Domain: homeobox homology <HOX>

Query Match          96.7%; Score 89; DB 2; Length 78;
Best Local Similarity 93.8%; Pred. No. 8e-07;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQIKWIFQNRRMKWKX 16
:|||||
Db 43 RQIKWIFQNRRMKWKX 58

RESULT 14
S47605
homeotic protein Hox-7 - Florida lancelet (fragment)
C/Species: Branchiostoma floridae (Florida lancelet)
C/Date: 01-Feb-1995 #sequence_revision 26-May-1995 #text_change 24-Sep-1999
C/Accession: S47605
R/Garcia-Fernandez, J.; Holland, P.W.H.
Nature 370, 563-566, 1994
A/Title: Archetypal organization of the amphioxus Hox gene cluster.
A/Reference number: S47599; MUID:94325179; PMID:7914353
A/Accession: S47605
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-81 <GAR>
A/Cross-references: EMBL:235147; NID:g520617; PIDN:CAA84519.1; PID:g520618
C/Superfamily: unassigned homeobox proteins; homeobox homology
C/Keywords: DNA binding; homeobox; nucleus; transcription regulation
F:4-60/Domain: homeobox homology <HOX>

Query Match          96.7%; Score 89; DB 2; Length 81;
Best Local Similarity 93.8%; Pred. No. 8.3e-07;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQIKWIFQNRRMKWKX 16
:|||||

```

Db 45 RQIKWQNRRMKWKK 60

RESULT 15

B29585
homeotic protein Hox 2.2 precursor - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 15-Dec-1988 #sequence_revision 30-Sep-1991 #text_change 17-Oct-1997
C/Accession: B29585
R/Lonai, P.; Arman, E.; Czosnek, H.; Ruddle, F.H.; Blatt, C.
DNA 6, 409-418, 1987
A>Title: New murine homeoboxes: structure, chromosomal assignment, and differential expression in adult erythropoiesis.
A/Reference number: A29585; MUID:88054465; PMID:2890503
A/Accession: B29585
A/Molecule type: DNA
A/Residues: 1-81 <LON>
A/Cross-references: GB:M18167
A/Note: the authors translated the codon CAG for residue 69 as Glu
C/Superfamily: unassigned homeobox proteins; homeobox homology
C/Keywords: DNA binding; homeobox; nucleus; transcription regulation
F:4-60/Domain: homeobox homology <HOX>

Query Match 96.7%; Score 89; DB 2; Length 81;
Best Local Similarity 93.8%; Pred. No. 8.3e-07;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQIKWQNRRMKWKK 16
Db 45 RQIKWQNRRMKWKK 60

Search completed: October 4, 2004, 18:58:26
Job time : 24.6322 secs

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QM protein - protein search, using sw model

Run on: October 4, 2004, 18:44:39 ; Search time 13.2174 Seconds
(without alignments)
63.032 Million cell updates/sec

Title: US-10-048-209-5
Perfect score: 92
Sequence: 1 RQIKWQNRRMKWKK 16
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	89	96.7	48	1 HXB6_XENLA	P31256 xenopus lae
2	89	96.7	49	1 HXA5_SHEEP	Q28599 ovis aries
3	89	96.7	71	1 HXA7_SHEEP	Q28600 ovis aries
4	89	96.7	71	1 HXC5_NOTVI	P31262 notophthalm
5	89	96.7	74	1 HM90_APIME	P15860 apis mellif
6	89	96.7	75	1 HXSA_SALSA	P09636 salmo salar
7	89	96.7	76	1 HXC4_RAT	P18865 rattus norv
8	89	96.7	78	1 HXA5_SALSA	P09637 salmo salar
9	89	96.7	80	1 HXA4_LINSA	P81192 lineus sang
10	89	96.7	81	1 HX5L_BRARE	P09013 brachydanio
11	89	96.7	82	1 HXB5_CHICK	P14838 gallus gall
12	89	96.7	84	1 HXB6_CHICK	P14839 gallus gall
13	89	96.7	86	1 SCR_APIME	P15859 apis mellif
14	89	96.7	87	1 HXC5_XENLA	P09020 xenopus lae
15	89	96.7	93	1 HXB8_PIG	P09078 sus scrofa
16	89	96.7	96	1 HXC6_BRARE	P15862 brachydanio
17	89	96.7	105	1 HXA7_RAT	P09634 rattus norv

18 89 96.7 105 1 HXB4 BRAPE
19 89 96.7 112 1 HXB7 RAT
20 89 96.7 148 1 HXA5 MAME
21 89 96.7 153 1 HXC6 SHEEP
22 89 96.7 208 1 HXA7 HEIFR
23 89 96.7 209 1 HXA7 HEIFR
24 89 96.7 217 1 HXB7 BOVIN
25 89 96.7 217 1 HXB7 HUMAN
26 89 96.7 217 1 HXB7 MOUSE
27 89 96.7 220 1 HXB7 XENLA
28 89 96.7 220 1 HXB7 XENLA
29 89 96.7 222 1 HXC5 HUMAN
30 89 96.7 222 1 HXC5 MOUSE
31 89 96.7 224 1 HXB6 HUMAN
32 89 96.7 224 1 HXB6 MOUSE
33 89 96.7 225 1 HXA7 MORA
34 89 96.7 228 1 HXB6 BRAPE
35 89 96.7 229 1 HXA6 HEIFR
36 89 96.7 229 1 HXA7 HEIFR
37 89 96.7 230 1 HXA7 HUMAN
38 89 96.7 230 1 HXB5 XENLA
39 89 96.7 232 1 HXA6 MOUSE
40 89 96.7 232 1 HXB4 XENLA
41 89 96.7 232 1 HXC5 BRAPE
42 89 96.7 233 1 HXA5 RAT
43 89 96.7 233 1 HXA6 HUMAN
44 89 96.7 234 1 HXC6 NOTVI
45 89 96.7 234 1 HXC6 XENLA

ALIGNMENTS

RESULT 1
HXB6_XENLA
ID HXB6_XENLA STANDARD; PRT; 48 AA.
AC P31256;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Homeobox protein Hox-B6 (XlHox-2.2) (Fragment).
GN HOXB6 OR XLHox-2.2.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93043517; PubMed=1384809;
RA Leroy P., de Robertis E.M.;
RT "Effects of lithium chloride and retinoic acid on the expression of
RT genes from the Xenopus laevis Hox 2 complex."
RL Dev. Dyn. 194;21-32(1992).
CC -!- FUNCTION: Sequence-specific transcription factor which is part of
CC a developmental regulatory system that provides cells with
CC specific positional identities on the anterior-posterior axis.

CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- SIMILARITY: Belongs to the Antp homeobox family.
CC
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CC
CC EMBL; M91587; AAA49750.1; -.
DR PIR; I51439; I51439.
DR InterPro; IPR001827; Antennapedia.
DR InterPro; IPR001356; Homeobox.
DR Pfam; PF00046; Homeobox; 1.
DR PRINTS; PR00024; HOMEBOX.
DR ProDom; PD000010; Homeobox; 1.
DR SMART; SM00389; Hox; 1.
DR PROSITE; PS00027; HOMEBOX 1; 1.
DR PROSITE; PS00032; ANTENNAPEDIA; PARTIAL.
DR PROSITE; PS00071; HOMEBOX 2; 1.
KW Homeobox; DNA-binding; Developmental protein; Nuclear protein;
KW Transcription regulation.
FT DNA_BIND <1 29 HOMEBOX.
FT NON_TER 1
SQ SEQUENCE 48 AA; 5716 MW; BC39E3682EDDD2A CRC64;
Query Match. 96.7%; Score 89; DB 1; Length 48;
Best Local similarity 93.8%; Pred. No. 7.5e-08;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KQIKWFQNRMRKWK 16
Db :|||||
12 RQIKWFQNRMRKWK 27
RESULT 2
HXA5_SHEEP
ID HXA5_SHEEP STANDARD; PRT; 49 AA.
AC Q28599;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Homeobox protein Hox-A5 (fragment).
GN HOXA5 OR HOXA-5.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RA Roche P.J.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
CC -!- FUNCTION: Sequence-specific transcription factor which is part of
CC a developmental regulatory system that provides cells with

CC specific positional identities on the anterior-posterior axis.
CC 5'-CYNATAATGTY-3'.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- SIMILARITY: Belongs to the Antp homeobox family.
CC
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CC
CC EMBL: U61978; AB04754.1; -.
CC HSSP: P02833; IHOM.
CC InterPro: IPR001356; Homeobox.
CC Pfam: PF00046; Homeobox; 1.
CC PRINTS: PR00024; HOMEBOX.
CC ProDom: PD000010; Homeobox; 1.
CC SMART: SM00389; HOX; 1.
CC PROSITE: PS00027; HOMEBOX_1; 1.
CC PROSITE: PS00071; HOMEBOX_2; 1.
CC Homeobox; DNA-binding; Developmental protein; Nuclear protein;
CC Transcription regulation.
CC KW NON_TER 1
CC FT DNA_BIND <1 49 HOMEBOX.
CC FT NON_TER 49
CC FT NON_TER 49
CC SQ SEQUENCE 49 AA; 6331 MW; 1EE702315E7C099B CRC64;

CC Query Match 96.7%; Score 89; DB 1; Length 49;
CC Best Local Similarity 93.8%; Pred. No. 7.7e-08;
CC Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

CC QY 1 KQIKWFOFNRKMKKK 16
CC Db :|||||
CC 32 RQIKWFOFNRKMKKK 47

CC RESULT 3
CC HXA7 SHEEP
CC ID HXA7 SHEEP STANDARD; PRT; 71 AA.
CC AC Q26600;
CC DT 01-NOV-1997 (Rel. 35, Created)
CC DT 01-NOV-1997 (Rel. 35, Last sequence update)
CC DT 28-FEB-2003 (Rel. 41, Last annotation update)
CC DE Homeobox protein Hox-A7 (Fragment).
CC GN HOXA7 OR HOXA-7.
CC OS Ovis aries (Sheep).
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
CC OC Bovidae; Caprinae; Ovis.
CC OX NCBI_TaxID=9940;
CC RN [1]
CC RP Roche P.J.;
CC RA SEQUENCE FROM N.A.
CC RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.

CC -!- FUNCTION: Sequence-specific transcription factor which is part of
CC a developmental regulatory system that provides cells with
CC specific positional identities on the anterior-posterior axis.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- SIMILARITY: Belongs to the Antp homeobox family.
CC
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CC
CC EMBL: U61979; AB04755.1; -.
CC HSSP: P02833; 9ANT.
CC InterPro: IPR001356; Homeobox.
CC Pfam: PF00046; Homeobox; 1.
CC PRINTS: PR00024; HOMEBOX.
CC ProDom: PD000010; Homeobox; 1.
CC SMART: SM00389; HOX; 1.
CC PROSITE: PS00027; HOMEBOX_1; 1.
CC PROSITE: PS00071; HOMEBOX_2; 1.
CC Homeobox; DNA-binding; Developmental protein; Nuclear protein;
CC Transcription regulation.
CC KW NON_TER 1
CC FT DNA_BIND 4 63 HOMEBOX.
CC FT NON_TER 71
CC FT NON_TER 71
CC SQ SEQUENCE 71 AA; 8888 MW; 931049FAC1BACE7 CRC64;

CC Query Match 96.7%; Score 89; DB 1; Length 71;
CC Best Local Similarity 93.8%; Pred. No. 1.1e-07;
CC Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

CC QY 1 KQIKWFOFNRKMKKK 16
CC Db :|||||
CC 46 RQIKWFOFNRKMKKK 61

CC RESULT 4
CC HXC5 NOTVI
CC ID HXC5 NOTVI STANDARD; PRT; 71 AA.
CC AC P31262;
CC DT 01-JUL-1993 (Rel. 26, Created)
CC DT 01-JUL-1993 (Rel. 26, Last sequence update)
CC DT 28-FEB-2003 (Rel. 41, Last annotation update)
CC DE Homeobox protein Hox-CS (NvHox-3.4) (Fragment).
CC OS Notothenchomus viridescens (Eastern newt) (Triturus viridescens).
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC OC Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae;
CC OC Notothenchomus.
CC OX NCBI_TaxID=6316;
CC RN [1]
CC RP
CC RA SEQUENCE FROM N.A.
CC RX MEDLINE=92290273; PubMed=1351019;

RA Belleville S., Beauchemin M., Tremblay M., Noiseux N., Savard P.;
 RT "Homeobox-containing genes in the newt are organized in clusters
 similar to other vertebrates.";
 RL Gene 114:179-186(1992).
 CC -!- FUNCTION: Sequence-specific transcription factor which is part of
 a developmental regulatory system that provides cells with
 specific positional identities on the anterior-posterior axis.
 CC -!- SUBCELLULAR LOCATION: Nuclear.
 CC -!- SIMILARITY: Belongs to the Antp homeobox family.
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 DR EMBL; M84001; AAA49397.1; ALT_INIT.
 DR PIR; JCI161; JCI161.
 DR HSP; P02833; 1SAN.
 DR InterPro; IPR001827; Antennapedia.
 DR InterPro; IPR001356; Homeobox.
 DR Pfam; PF00046; homeobox; 1.
 DR PRINTS; PR00024; HOMEBOX.
 DR ProDom; PD000010; Homeobox; 1.
 DR SMART; SM00389; Hox; 1.
 DR PROSITE; PS00027; HOMEBOX_1; 1.
 DR PROSITE; PS00032; ANTENAPEDIA; PARTIAL.
 DR PROSITE; PS00071; HOMEBOX_2; 1.
 KW Homeobox; DNA-binding; Developmental protein; Nuclear protein;
 KW Transcription regulation.
 FT NON_TER 1 1
 FT DNA_BIND 4 63 HOMEBOX.
 FT NON_TER 71 71
 FT NON_TER 71 71
 SQ SEQUENCE 71 AA; 8979 MW; 07999FDE8995B42 CRC64;

Query Match 96.7%; Score 89; DB 1; Length 71;
 Best Local Similarity 93.8%; Pred. No. 1.1e-07;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KQKIWFQNRNRKWK 16
 :|||||
 Db 46 RQKIWFQNRNRKWK 61

RESULT 5
 HM90_APIME
 ID HM90_APIME STANDARD; PRT; 74 AA.
 AC P15860;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Homeobox protein H90 (Fragment).
 OS Apis mellifera (Honeybee).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;

OC Apidae; Apis.
 OX NCBI_taxID=7460;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90099384; PubMed=2574865;
 RA Walldorf U., Fleig R., Gehring W.J.;
 RT "Comparison of homeobox-containing genes of the honeybee and
 Drosophila.";
 RL Proc. Natl. Acad. Sci. U.S.A. 86:9971-9975(1989).
 CC -!- SUBCELLULAR LOCATION: Nuclear (potential).
 CC -!- SIMILARITY: Belongs to the Antp homeobox family.
 CC -!- SIMILARITY: Contains 1 homeobox domain.
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 CC -----
 DR EMBL; M29493; AAA27728.1; -.
 DR PIR; D34510; D34510.
 DR HSP; P02833; 1HOM.
 DR InterPro; IPR001356; Homeobox.
 DR Pfam; PF00046; homeobox; 1.
 DR PRINTS; PR00024; HOMEBOX.
 DR ProDom; PD000010; Homeobox; 1.
 DR SMART; SM00389; Hox; 1.
 DR PROSITE; PS00027; HOMEBOX_1; 1.
 DR PROSITE; PS00071; HOMEBOX_2; 1.
 KW Homeobox; DNA-binding; Developmental protein; Nuclear protein.
 FT NON_TER 1 1
 FT DNA_BIND 8 67 HOMEBOX.
 FT NON_TER 74 74
 FT NON_TER 74 74
 SQ SEQUENCE 74 AA; 9263 MW; 5FC8FB4F723D3837 CRC64;

Query Match 96.7%; Score 89; DB 1; Length 74;
 Best Local Similarity 93.8%; Pred. No. 1.2e-07;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KQKIWFQNRNRKWK 16
 :|||||
 Db 50 RQKIWFQNRNRKWK 65

RESULT 6
 HMSA_SALSA
 ID HMSA_SALSA STANDARD; PRT; 75 AA.
 AC P09636;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Homeobox protein SL2-A (Fragment).
 OS Salmo salar (Atlantic salmon).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;

OC Protecanthopterygii; Salmoniformes; Salmonidae; Salmo.
 OX NCBI_TaxID=8030;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=88226009; PubMed=2897318;
 RA Fjose A., Molven A., Eiken H.G.;
 RT Molecular cloning and characterization of homeo-box-containing genes
 RT from Atlantic salmon."
 RL Gene 621141-152(1988).
 CC -|- SUBCELLULAR LOCATION: Nuclear (Probable).
 CC -|- SIMILARITY: Belongs to the Antp homeobox family.
 CC -|- SIMILARITY: Contains 1 homeobox domain.
 CC -----
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 CC -----
 DR EMBL; M18903; AAA49559.1; -.
 DR PIR; I51341; I51341.
 DR HSSP; P02833; 9ANT.
 DR InterPro; IPR001356; Homeobox.
 DR Pfam; PF00046; Homeobox; 1.
 DR PRINTS; PR00024; HOMEBOX.
 DR ProDom; PD00010; Homeobox; 1.
 DR SMART; SM00389; HOX; 1.
 DR PROSITE; PS00027; HOMEBOX_1; 1.
 DR PROSITE; PS00071; HOMEBOX_2; 1.
 DR ProDom; PD00010; Homeobox; 1.
 DR PRINTS; PR00024; HOMEBOX.
 DR PRINTS; PR00031; HTHREPRESSR.
 DR ProDom; PD00010; Homeobox; 1.
 DR SMART; SM00389; HOX; 1.
 DR PROSITE; PS00032; ANTENNAPEDIA; PARTIAL.
 DR PROSITE; PS00027; HOMEBOX_1; 1.
 DR PROSITE; PS00071; HOMEBOX_2; 1.
 KW Homeobox; DNA-binding; Developmental protein; Nuclear protein;
 FT NON_TER 1 1
 FT DNA_BIND 1 60 HOMEBOX.
 FT NON_TER 75 75
 SQ SEQUENCE 75 AA; 9330 MW; FC02C3672F35475D CRC64;

 Query Match 96.7%; Score 89; DB 1; Length 75;
 Best Local Similarity 93.8%; Pred. No. 1.2e-07;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

 OY 1 KQIKWIFQNRKMKWK 16
 :|||||
 DB 43 RQIKWIFQNRKMKWK 58

 RESULT 7
 ID HKX4 RAT STANDARD; PRT; 76 AA.
 AC P18565;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Homeobox protein Hox-c4 (R3) (Fragment).
 GN HOXC4 OR HOXC-4.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley;
 RA MEDLINE=89231502; PubMed=2907739;
 RA Falzon M., Chung S.Y.;
 RT "The expression of rat homeobox-containing genes is developmentally
 RT regulated and tissue specific."
 RL Development 103:601-610(1988).
 CC -|- FUNCTION: Sequence-specific transcription factor which is part of
 CC a developmental regulatory system that provides cells with
 CC specific positional identities on the anterior-posterior axis.
 CC -|- SUBCELLULAR LOCATION: Nuclear.
 CC -|- TISSUE SPECIFICITY: Predominantly spinal cord and kidney.
 CC -|- SIMILARITY: Belongs to the Antp homeobox family. Deformed
 CC subfamily.
 CC -----
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 CC -----
 DR EMBL; M37567; AAA41343.1; -.
 DR PIR; C43559; C43559.
 DR HSSP; P02833; 9ANT.
 DR InterPro; IPR001827; Antennapedia.
 DR InterPro; IPR001356; Homeobox.
 DR InterPro; IPR000047; HTH_lambrepresr.
 DR Pfam; PF00046; homeobox; 1.
 DR PRINTS; PR00024; HOMEBOX.
 DR PRINTS; PR00031; HTHREPRESSR.
 DR ProDom; PD00010; Homeobox; 1.
 DR SMART; SM00389; HOX; 1.
 DR PROSITE; PS00032; ANTENNAPEDIA; PARTIAL.
 DR PROSITE; PS00027; HOMEBOX_1; 1.
 DR PROSITE; PS00071; HOMEBOX_2; 1.
 KW Homeobox; DNA-binding; Developmental protein; Nuclear protein;
 FT NON_TER 1 1
 FT DNA_BIND 11 70 HOMEBOX.
 FT NON_TER 70 70
 SQ SEQUENCE 76 AA; 9293 MW; 5235f665c0672385 CRC64;

 Query Match 96.7%; Score 89; DB 1; Length 76;
 Best Local Similarity 93.8%; Pred. No. 1.2e-07;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

 OY 1 KQIKWIFQNRKMKWK 16
 :|||||
 DB 53 RQIKWIFQNRKMKWK 68

 RESULT 8
 HXA5_SALSA

ID HXA5 SALSA STANDARD; PRT; 78 AA.
AC P0967;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Homeobox protein Hox-A5 (512-B) (Fragment).
GN HXA5.
OS Salmo salar (Atlantic salmon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
OX NCBI_TaxID=8030;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88226009; PubMed=2897318;
RA Fjose A., Molven A., Eiken H.G.;
RT "Molecular cloning and characterization of homeo-box-containing genes
from Atlantic salmon";
RL Gene 62141-152(1988).
CC -!- FUNCTION: Sequence-specific transcription factor which is part of
a developmental regulatory system that provides cells with
specific positional identities on the anterior-posterior axis.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- SIMILARITY: Belongs to the Antp homeobox family.
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DR PIR; M18904; AAA49560.1; -.
DR PIR; I51342; I51342.
DR HSSP; P02833; 9ANT.
DR InterPro; IPR001827; Antennapedia.
DR InterPro; IPR001356; Homeobox.
DR Pfam; PF00046; homeobox; 1.
DR PRINTS; P00024; HOMEBOX.
DR ProDom; PD000010; Homeobox; 1.
DR SMART; SMO0389; HOX; 1.
DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; PS00032; ANTENAPEDIA; PARTIAL.
DR PROSITE; PS00071; HOMEBOX_2; 1.
KW Homeobox; DNA-binding; Developmental protein; Nuclear protein;
KW Transcription regulation.
FT NON_TER 1 1
FT DNA_BIND 1 60 HOMEBOX.
SQ SEQUENCE 78 AA; 9489 MW; 828DEDDF78AC820 CRC64;
Query Match 96.7%; Score 89; DB 1; Length 78;
Best Local Similarity 93.8%; Pred. No. 1.3e-07;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KQIKIWFQNRNRKWK 16
:|||||

Db 43 RQIKIWFQNRNRKWK 58
RESULT 9
HXA4 LINSA
ID HXA4 LINSA STANDARD; PRT; 80 AA.
AC P81192;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Homeobox protein Hox-A4 (LsHox 4) (Fragment).
GN HXA4.
OS Lineus sanguineus (Ribbon worm).
OC Eukaryota; Metazoa; Nemertea; Annelida; Heteronemertea; Lineidae;
OC Lineus.
OX NCBI_TaxID=48190;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98169491; PubMed=9301210;
RA Knita-Cunisse M., Locsi F., Bierre J., Gehring W.J.;
RT "Homeobox genes in the ribbon-worm Lineus sanguineus: evolutionary
implications";
RL Proc. Natl. Acad. Sci. U.S.A. 95:3030-3035(1998).
CC -!- FUNCTION: Sequence-specific transcription factor which is part of
a developmental regulatory system that provides cells with
specific positional identities on the anterior-posterior axis (By
similarity).
CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -!- SIMILARITY: Belongs to the Antp homeobox family. Deformed
subfamily.
DR HSSP; P02833; 9ANT.
DR InterPro; IPR001827; Antennapedia.
DR InterPro; IPR001356; Homeobox.
DR InterPro; IPR000047; HTH_lamb-repressr.
DR Pfam; PF00046; homeobox; 1.
DR PRINTS; P00024; HOMEBOX.
DR PRINTS; P00031; HTHREPRESSR.
DR ProDom; PD000010; Homeobox; 1.
DR SMART; SMO0389; HOX; 1.
DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; PS00071; HOMEBOX_2; 1.
DR PROSITE; PS00032; ANTENAPEDIA; PARTIAL.
KW Homeobox; DNA-binding; Developmental protein; Nuclear protein;
KW Transcription regulation.
FT NON_TER 1 1
FT DNA_BIND 21 80 HOMEBOX.
FT NON_TER 80 80
SQ SEQUENCE 80 AA; 9860 MW; F2CE1B01CB8042F1 CRC64;
Query Match 96.7%; Score 89; DB 1; Length 80;
Best Local Similarity 93.8%; Pred. No. 1.3e-07;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KQIKIWFQNRNRKWK 16
:|||||

Db 53 RQIKIWFQNRNRKWK 68

48 RQIKWFWQRMRWKX 63

RESULT 10

HXSL_BRARE STANDARD; PRT; 81 AA.
AC P05013;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Homeobox protein Hox-B5 like (ZF-54) (Fragment).
GN HOXB5 OR ZF54 OR ZF-54.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89016617; PubMed=2902590;
RA Njolstad P.R., Molven A., Hordvik I., Apold J., Fjose A.;
RT "Primary structure, developmentally regulated expression and potential duplication of the zebrafish homeobox gene ZF-21.";
RL Nucleic Acids Res. 16:9097-9113(1988).
CC -!- FUNCTION: Sequence-specific transcription factor which is part of a developmental regulatory system that provides cells with specific positional identities on the anterior-posterior axis.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- SIMILARITY: Belongs to the Antp homeobox family.

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EMBL; X12803; CAA31291.1; -.
DR HSSP; P02833; 1SAN.
DR ZFIN; ZDB-GENE-000823-6; hoxb5b.
DR InterPro; IPR001356; Homeobox.
DR Pfam; PF00046; homeobox; 1.
DR ProDom; PD000010; Homeobox; 1.
DR SMART; SMO0389; HOX; 1.
DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; PS00071; HOMEBOX_2; 1.
KW Homeobox; DNA-binding; Developmental protein; Nuclear protein;
Transcription regulation.
FT NON_TER 1 1
FT DNA_BIND 6 65 HOMEBOX.
SQ SEQUENCE 81 AA; 9977 MW; B7698AEFF3C6B4 CRC64;

Query Match 96.7%; Score 89; DB 1; Length 81;
Best Local Similarity 93.8%; Pred. No. 1.3e-07;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 RQIKWFWQRMRWKX 16

48 RQIKWFWQRMRWKX 63

RESULT 11

HXSL_BRARE STANDARD; PRT; 82 AA.
AC P14835;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Homeobox protein Hox-B5 (Glox-2.1) (Fragment).
GN HOXB5 OR GLOX-2.1.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90126373; PubMed=2575515;
RA Wedden S.E., Fang K., Eichele G.;
RT "Expression pattern of homeobox-containing genes during chick embryogenesis.";
RL Development 105:639-650(1989).
CC -!- FUNCTION: Sequence-specific transcription factor which is part of a developmental regulatory system that provides cells with specific positional identities on the anterior-posterior axis.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- SIMILARITY: Belongs to the Antp homeobox family.

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EMBL; X16846; CAA34743.1; -.
DR PIR; S08302; S08302.
DR HSSP; P02833; 1SAN.
DR InterPro; IPR001827; Antennapedia.
DR InterPro; IPR001356; Homeobox.
DR Pfam; PF00046; homeobox; 1.
DR PRINTS; PR00024; HOMEBOX.
DR ProDom; PD000010; Homeobox; 1.
DR SMART; SMO0389; HOX; 1.
DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; PS00032; ANTENNAPEDIA; PARTIAL.
DR PROSITE; PS00071; HOMEBOX_2; 1.
KW Homeobox; DNA-binding; Developmental protein; Nuclear protein;
Transcription regulation.
FT NON_TER 1 1
FT DNA_BIND 7 66 HOMEBOX.
SQ SEQUENCE 82 AA; 9877 MW; 53F70ACDC9FDF8F CRC64;

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EMBL; X16846; CAA34743.1; -.
DR PIR; S08302; S08302.
DR HSSP; P02833; 1SAN.
DR InterPro; IPR001827; Antennapedia.
DR InterPro; IPR001356; Homeobox.
DR Pfam; PF00046; homeobox; 1.
DR PRINTS; PR00024; HOMEBOX.
DR ProDom; PD000010; Homeobox; 1.
DR SMART; SMO0389; HOX; 1.
DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; PS00032; ANTENNAPEDIA; PARTIAL.
DR PROSITE; PS00071; HOMEBOX_2; 1.
KW Homeobox; DNA-binding; Developmental protein; Nuclear protein;
Transcription regulation.
FT NON_TER 1 1
FT DNA_BIND 7 66 HOMEBOX.
SQ SEQUENCE 82 AA; 9877 MW; 53F70ACDC9FDF8F CRC64;

DR PROSITE; PS00027; HOMEBOX 1; 1.
DR PROSITE; PS00032; ANTENNAPEDIA; PARTIAL.
DR PROSITE; PS00071; HOMEBOX 2; 1.
KW Homeobox; DNA-binding; Developmental protein; Nuclear protein;
KW Transcription regulation.
FT NON_TER 1 1
FT DNA_BIND 7 66 HOMEBOX
SQ SEQUENCE 84 AA; 10279 MW; BC06E10165B19E71 CRC64;
Query Match 96.7%; Score 89; DB 1; Length 82;
Best Local Similarity 93.8%; Pred. No. 1.3e-07;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KOIKWFOQRNRKWK 16
Db 49 RQIKWFOQRNRKWK 64
RESULT 12
HX86_CHICK STANDARD; PRT; 84 AA.
AC P14839;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Homeobox protein Hox-B6 (HBOX-2.2) (Fragment).
GN HBOX6 OR HBOX-2.2.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Erythrocyte;
RX MEDLINE=90126373; PubMed=2575515;
RA Wedden S.E., Pang K., Eichele G.;
RT "Expression pattern of homeobox-containing genes during chick
embryogenesis";
RL Development 105:639-650(1989).
CC -!- FUNCTION: Sequence-specific transcription factor which is part of
a developmental regulatory system that provides cells with
specific positional identities on the anterior-posterior axis.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- SIMILARITY: Belongs to the Antp homeobox family.
CC
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CC
CC EMBL; X16847; CAA34744.1; -.
CC PIR; S08303; S08303.
CC HSSP; P02833; LHOM.
CC InterPro; IPR001827; Antennapedia.
CC InterPro; IPR001356; Homeobox.
CC Pfam; PF00046; homeobox; 1.
CC PRINTS; PR00024; HOMEBOX.
CC PRINTS; PR00031; HTHREPRESSR.
CC ProDom; PD000010; Homeobox; 1.
CC SMART; SM00389; HOK; 1.

DR PROSITE; PS00027; HOMEBOX 1; 1.
DR PROSITE; PS00032; ANTENNAPEDIA; PARTIAL.
DR PROSITE; PS00071; HOMEBOX 2; 1.
KW Homeobox; DNA-binding; Developmental protein; Nuclear protein;
KW Transcription regulation.
FT NON_TER 1 1
FT DNA_BIND 7 66 HOMEBOX
SQ SEQUENCE 84 AA; 10279 MW; BC06E10165B19E71 CRC64;
Query Match 96.7%; Score 89; DB 1; Length 84;
Best Local Similarity 93.8%; Pred. No. 1.4e-07;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KOIKWFOQRNRKWK 16
Db 49 RQIKWFOQRNRKWK 64
RESULT 13
SCR_APIME STANDARD; PRT; 86 AA.
AC P15859;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Homeobox protein H55 (Fragment).
DE Apis mellifera (Honeybee).
OS Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
OC Apidae; Apis.
OX NCBI_TaxID=7460;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9009384; PubMed=2574865;
RA Walldorf U., Fleig R., Gehring W.J.;
RT "Comparison of homeobox-containing genes of the honeybee and
Drosophila";
RL Proc. Natl. Acad. Sci. U.S.A. 86:9971-9975(1989).
CC -!- FUNCTION: Sequence-specific transcription factor which is part of
a developmental regulatory system that provides cells with
specific positional identities on the anterior-posterior axis.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- SIMILARITY: BELONGS TO THE ANTP HOMEBOX FAMILY. STRONGEST, TO SCR
OF DROSOPHILA.
CC
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CC
CC EMBL; M29488; AAA27723.1; -.
CC PIR; A34510; A34510.
CC HSSP; P02833; LSAN.
CC InterPro; IPR001827; Antennapedia.

DR InterPro: IPR001356; Homeobox.
 DR Pfam: PF00046; Homeobox; 1.
 DR PRINTS: PS00024; HOMEBOX.
 DR PRODOM: PDC00010; Homeobox; 1.
 DR SMART: SMO0389; Hox; 1.
 DR PROSITE: PS00032; ANTENNAPEDIA; PARTIAL.
 DR PROSITE: PS00027; HOMEBOX 1; 1.
 DR PROSITE: PS00071; HOMEBOX 2; 1.
 DR Homeobox; DNA-binding; Developmental protein; Nuclear protein.
 FT NON_TER 1 1
 FT DNA_BIND 8 67 HOMEBOX.
 FT NON_TER 86 86
 SQ SEQUENCE 86 AA; 10713 MW; 2A49AB857C138AB8 CRC64;

Query Match 96.7%; Score 89; DB 1; Length 86;
 Best Local Similarity 93.8%; Pred. No. 1.4e-07;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQIKWIFQNRRMKWK 16
 :|||||
 Db 50 RQIKWIFQNRRMKWK 65

RESULT 14
 HKCS_XENIA STANDARD; PRT; 87 AA.
 AC P09020;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Homeobox protein Hox-C5 (XlHox-5) (Fragment).
 GN HOXC5 OR XLHOBX.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;
 CC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88157707; PubMed=2894634;
 RA Fritz A., de Robertis E.M.;
 RT "Xenopus homeobox-containing cDNAs expressed in early development."
 RL Nucleic Acids Res. 16:1453-1469(1988).
 CC -!- FUNCTION: Sequence-specific transcription factor which is part of
 a developmental regulatory system that provides cells with
 specific positional identities on the anterior-posterior axis.
 CC -!- SUBCELLULAR LOCATION: Nuclear.
 CC -!- DEVELOPMENTAL STAGE: EXPRESSED EXCLUSIVELY IN EARLY EMBRYOS.
 CC -!- SIMILARITY: Belongs to the Antp homeobox family.
 CC
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CC EMBL: X07105; CAA30126.1; -
 DR PIR: S00589; S00589.
 DR RSP: P02833; PANT.
 DR TRANSFAC: T03765; -
 DR InterPro: IPR001827; Antennapedia.
 DR InterPro: IPR001356; Homeobox.
 DR Pfam: PF00046; homeobox; 1.
 DR PRINTS: PS00025; ANTENNAPEDIA.
 DR PRINTS: PS00024; HOMEBOX.
 DR PRODOM: PDC00010; Homeobox; 1.
 DR SMART: SMO0389; Hox; 1.
 DR PROSITE: PS00027; HOMEBOX 1; 1.
 DR PROSITE: PS00032; ANTENNAPEDIA; 1.
 DR PROSITE: PS00071; HOMEBOX 2; 1.
 KW Homeobox; DNA-binding; Developmental protein; Nuclear protein;
 KW Transcription regulation.
 FT NON_TER 1 1
 FT SITE 5 10 ANTP-TYPE HEXAPEPTIDE.
 FT DNA_BIND 20 79 HOMEBOX.
 FT NON_TER 87 87
 SQ SEQUENCE 87 AA; 11058 MW; E67939E334E2BA43 CRC64;

Query Match 96.7%; Score 89; DB 1; Length 87;
 Best Local Similarity 93.8%; Pred. No. 1.4e-07;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQIKWIFQNRRMKWK 16
 :|||||
 Db 62 RQIKWIFQNRRMKWK 77

RESULT 15
 HXB8_PIG STANDARD; PRT; 93 AA.
 ID HXB8_PIG
 AC P09078;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Homeobox protein Hox-B8 (Hox-2.4) (Fragment).
 GN HOXB8 OR HOBX-2.4.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9623;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89057478; PubMed=2904133;
 RA Miller J.R., Gaunt S.J., Sharpe P.T.;
 RT "Pig Hox-2.4 has accumulated a frameshift mutation relative to mouse
 Hox-2.4."
 RL Nucleic Acids Res. 16:10364-10364(1988).
 CC -!- FUNCTION: Sequence-specific transcription factor which is part of
 a developmental regulatory system that provides cells with
 specific positional identities on the anterior-posterior axis.
 CC -!- SUBCELLULAR LOCATION: Nuclear.
 CC -!- SIMILARITY: Belongs to the Antp homeobox family.
 CC

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CC or send an email to license@isb-sib.ch).
CC -----

DR EMBL; X06668; CAB57825.1; ALT_SEQ.
DR HSSP; P02834; LB81.
DR InterPro; IPR001827; Antennapedia.
DR InterPro; IPR001356; Homeobox.
DR InterPro; IPR000047; HTH_lambdarepressor.
DR Pfam; PF00046; homeobox; 1.
DR PRINTS; PRO0024; HOMEBOX.
DR PRINTS; PRO0031; HTHREPRESSR.
DR ProDom; PD000010; Homeobox; 1.
DR SMART; SM00389; HOK; 1.
DR PROSITE; PS00032; ANTENNAPEDIA; PARTIAL.
DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; PS00071; HOMEBOX_2; 1.
KW Homeobox; DNA-binding; Developmental protein; Nuclear protein;
KW Transcription regulation.
FT NON_TER 1 1
FT DNA_BIND 7 66 HOMEBOX.
SQ SEQUENCE 93 AA; 10672 MW; 7841DD6D176345EC CRC64;

Query Match 96.7%; Score 89; DB 1; Length 93;
Best Local Similarity 93.8%; Pred. No. 1.5e-07;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KQIKIWFQNRMRKWK 16
:|||||
Db 49 RQIKIWFQNRMRKWK 64

Search completed: October 4, 2004, 18:57:19
Job time : 14.2174 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 4, 2004, 18:37:37 ; Search time 75.8261 Seconds
(without alignments)
66.577 Million cell updates/sec

Title: US-10-048-209-5
Perfect score: 92
Sequence: 1 KQIKIWFQNRMRKWK 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25:
1: sp_archaea:
2: sp_bacteria:
3: sp_fungi:
4: sp_human:
5: sp_invertebrate:
6: sp_mammal:
7: sp_mnc:
8: sp_organelle:
9: sp_phage:
10: sp_plant:
11: sp_rodent:
12: sp_virus:
13: sp_vertebrate:
14: sp_unclassified:
15: sp_rvirus:
16: sp_bacteriap:
17: sp_archaeap:

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query	Match	Length	DB	ID	Description
--------	-------	-------	-------	--------	----	----	-------------

1 90 97.8 190 5 Q9NLA0 Q9nla0 podocoryne
2 89 96.7 33 5 Q86FU0 Q86fu0 drosophila
3 89 96.7 39 13 Q57368 Q57368 brachydanio
4 89 96.7 42 11 Q80WH6 Q80wh6 rattus sp.
5 89 96.7 43 13 Q57359 Q57359 brachydanio
6 89 96.7 46 13 Q9PVR9 Q9pvr9 oryzias lat
7 89 96.7 51 5 Q27413 Q27413 ctendrilus
8 89 96.7 51 5 Q23743 Q23743 ctendrilus
9 89 96.7 51 5 Q26407 Q26407 ctendrilus
10 89 96.7 57 13 Q9PVR8 Q9pvr8 oryzias lat
11 89 96.7 58 5 Q9Y188 Q9y188 priapulus c
12 89 96.7 58 5 Q25208 Q25208 junonia coe
13 89 96.7 58 13 Q57362 Q57362 brachydanio
14 89 96.7 59 5 Q8WFM9 Q8wfm9 lithobius a
15 89 96.7 59 5 Q9NE42 Q9ne42 anopheles g
16 89 96.7 59 13 Q9PVR5 Q9pvr5 oryzias lat
17 89 96.7 60 5 Q77143 Q77143 archeogzete
18 89 96.7 60 5 Q77139 Q77139 archeogzete
19 89 96.7 60 11 Q80WH7 Q80wh7 rattus sp.
20 89 96.7 60 11 Q80WH4 Q80wh4 rattus sp.
21 89 96.7 60 13 Q8QGL5 Q8qgl5 petromyzon
22 89 96.7 60 13 Q8QGL3 Q8qgl3 petromyzon
23 89 96.7 60 13 Q8QGL6 Q8qgl6 petromyzon
24 89 96.7 60 13 Q8QGL2 Q8qgl2 petromyzon
25 89 96.7 60 13 Q8QGL8 Q8qgl8 petromyzon
26 89 96.7 60 13 Q8QGL7 Q8qgl7 petromyzon
27 89 96.7 61 5 Q27910 Q27910 polyanarca
28 89 96.7 63 5 Q77138 Q77138 archeogzete
29 89 96.7 63 5 Q8WXB2 Q8wxb2 holopneuste
30 89 96.7 66 13 Q57356 Q57356 brachydanio
31 89 96.7 69 5 Q9U9T4 Q9u9t4 nereis vire
32 89 96.7 69 5 Q9BMF7 Q9bm7 haliotis as
33 89 96.7 70 5 Q96TW5 Q96tw5 folcomia ca
34 89 96.7 70 13 Q801B4 Q801b4 latimeria m
35 89 96.7 71 13 Q9PVS3 Q9pvs3 oryzias lat
36 89 96.7 71 13 Q9PVS1 Q9pval oryzias lat
37 89 96.7 73 5 Q9Y186 Q9y186 priapulus c
38 89 96.7 73 5 Q86D93 Q86d93 spadella ce
39 89 96.7 74 13 Q57367 Q57367 brachydanio
40 89 96.7 75 5 Q25209 Q25209 junonia coe
41 89 96.7 75 13 Q9PVR6 Q9pvr6 oryzias lat
42 89 96.7 76 5 Q44257 Q44257 ethmostigmu
43 89 96.7 76 5 Q86NB1 Q86nb1 calanus hel
44 89 96.7 77 5 Q44260 Q44260 ethmostigmu
45 89 96.7 77 5 Q9Y187 Q9y187 priapulus c

ALIGNMENTS

RESULT 1
Q9NLA0 Q9NLA0 PRELIMINARY; PRT; 190 AA.
AC Q9NLA0;
DT 01-OCT-2000 (TRENBLrel. 15, Created)
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)

DE Cnox2-Pc.
GN CNOX2-PC.
OS Podocoryne carnea.
OC Eukaryota; Metazoa; Onidaria; Hydrozoa; Hydroida; Anthomedusae;
OC Hydractiniidae; Podocoryne.
OX NCBI_TaxID=6096;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21110504; PubMed=1180816;
RA Masuda-Nakagawa L.M., Gieger H., Aerne B.L., Schmid V.;
RT "The CNOX2-like gene Cnox2-Pc is expressed at the anterior region in all
RL life cycle stages of the jellyfish Podocoryne carnea.";
CC Dev. Genes Evol. 210:151-156(2000).
CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
DR ENBL; AB014684; BAA94091.1; -.
DR HSSP; P14653; 1B72.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:00003700; F:transcription factor activity; IEA.
DR GO; GO:00006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR001356; Homeobox.
DR InterPro; IPR000047; HTH_lambdarepressr.
DR Pfam; PF00046; homeobox; 1.
DR PRINTS; PR00024; HOMEBOX.
DR PRINTS; PR00031; HTHREPRESSR.
DR ProDom; PD000010; Homeobox; 1.
DR SMART; SMC0389; HOX; 1.
DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; PS50071; HOMEBOX_2; 1.
KW DNA-binding; Homeobox; Nuclear protein.
SQ SEQUENCE 190 AA; 22929 MW; A476A14D9147288A CRC64;
Query Match 97.8%; Score 90; DB 5; Length 190;
Best Local Similarity 87.5%; Pred. No. 1.6e-06;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 KQKIWFQNRKWKX 16
DB 161 KQKVFQNRKWKX 176
RESULT 2
Q86FU0 Q86FU0 PRELIMINARY; PRT; 33 AA.
ID Q86FU0;
AC Q86FU0;
DT 01-JUN-2003 (TRENBLrel. 24, Created)
DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Antennapedia complex (Fragment).
GN ANT-C.
OS Drosophila pseudoobscura (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7237;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93292933; PubMed=8099892;

RA Randazzo F.M., Seeger M.A., Hues C.A., Sweeney M.A., Cecil J.K., Kaufman T.C.;
 RT "Structural changes in the antennapedia complex of *Drosophila pseudobscura*.";
 RL Genetics 134:319-330(1993).
 DR EMBL: S63455; AAPI3946.1; -.
 DR GO: GO:0005634; C:nucleus; IEA.
 DR GO: GO:0003700; F:transcription factor activity; IEA.
 DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro: IPR001356; Homeobox.
 DR PRINTS; PR00024; HOMEBOX.
 DR ProDom: PD00010; Homeobox; 1.
 DR PROSITE; PS50071; HOMEBOX_2; 1.
 FT NON_TER 1 1
 FT NON_TER 33 33
 FT NON_TER 33 33
 SQ SEQUENCE 33 AA; 3963 MW; D78E37ED81FD45DF CRC64;
 Query Match 96.7%; Score 89; DB 5; Length 33;
 Best Local Similarity 93.8%; Pred. No. 4.1e-07;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KQIKIWFQNRMRKWK 16
 Db 7 RQIKIWFQNRMRKWK 22
 RESULT 3
 OS7368 PRELIMINARY; PRT; 39 AA.
 ID OS7368 PRELIMINARY; PRT; 39 AA.
 AC OS7368 PRELIMINARY; PRT; 39 AA.
 DT 01-JUN-1998 (TRENBLrel. 06, Created)
 DT 01-JUN-1998 (TRENBLrel. 06, Last sequence update)
 DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
 DE Hox5 protein (Fragment).
 GN Hox5A OR HOXC5.
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7935;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Prince V.E., Joly L., Ekker M., Ho R.K.;
 RT "Zebrafish hox genes: genomic organization and modified colinear expression patterns in the trunk.";
 RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
 CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 DR EMBL: Y14539; CAA74874.1; -.
 DR ZFIN: ZDB-GENE-980526-533; hoxc5a.
 DR GO: GO:0005634; C:nucleus; IEA.
 DR GO: GO:0003700; F:transcription factor activity; IEA.
 DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro: IPR001356; Homeobox.
 DR Pfam: PF00046; homeobox; 1.
 DR PRINTS; PR00024; HOMEBOX.
 DR PRINTS; PR00031; HTHREPRESSR.

DR ProDom: PD00010; Homeobox; 1.
 DR SMART; SM00389; HOX; 1.
 DR PROSITE; PS00027; HOMEBOX_1; 1.
 DR PROSITE; PS00071; HOMEBOX_2; 1.
 KW DNA-binding; Homeobox; Nuclear protein.
 FT NON_TER 1 1
 FT NON_TER 39 39
 SQ SEQUENCE 39 AA; 4827 MW; 592A0FEC12E59860 CRC64;
 Query Match 96.7%; Score 89; DB 13; Length 39;
 Best Local Similarity 93.8%; Pred. No. 4.8e-07;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KQIKIWFQNRMRKWK 16
 Db 14 RQIKIWFQNRMRKWK 29
 RESULT 4
 OS7368 PRELIMINARY; PRT; 42 AA.
 ID OS7368 PRELIMINARY; PRT; 42 AA.
 AC OS7368 PRELIMINARY; PRT; 42 AA.
 DT 01-JUN-2003 (TRENBLrel. 24, Created)
 DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
 DE Hox-A1Hox-1 (Fragment).
 GN Hox-A1Hox-1.
 OS Rattus sp.
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10118;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Sakoyama Y., Mizuta I., Ogasawara N., Yoshikawa H.;
 RT "Cloning of rat homeobox genes.";
 RL Biochem. Genet. 32:351-360(1994).
 DR EMBL: S76290; AAP31864.1; -.
 DR GO: GO:0005634; C:nucleus; IEA.
 DR GO: GO:0003700; F:transcription factor activity; IEA.
 DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro: IPR001356; Homeobox.
 DR Pfam: PF00046; homeobox; 1.
 DR PRINTS; PR00024; HOMEBOX.
 DR PRINTS; PR00031; HTHREPRESSR.
 DR ProDom: PD00010; Homeobox; 1.
 DR SMART; SM00389; HOX; 1.
 DR PROSITE; PS00027; HOMEBOX_1; 1.
 DR PROSITE; PS00071; HOMEBOX_2; 1.
 FT NON_TER 1 1
 FT NON_TER 42 42
 FT NON_TER 42 42
 SQ SEQUENCE 42 AA; 5494 MW; 38E5153B92216FE9 CRC64;
 Query Match 96.7%; Score 89; DB 11; Length 42;
 Best Local Similarity 93.8%; Pred. No. 5.2e-07;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQIKWIFQNRMRKWKX 16
 Db 25 RQIKWIFQNRMRKWKX 40

RESULT 5
 OS7359 PRELIMINARY; PRT; 43 AA.
 AC OS7359;
 DT 01-JUN-1998 (TRENBLrel. 06, Created)
 DT 01-JUN-1998 (TRENBLrel. 06, Last sequence update)
 DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
 DE Hox5 protein (Fragment).
 GN HOB55 OR HOBX5.
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Prince V.E., Joly L., Ekker M., Ho R.K.;
 RT "Zebrafish hox genes: genomic organization and modified colinear
 expression patterns in the trunk."
 RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
 CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 DR EMBL; Y14526; CAA74861.1; -.
 DR ZFIN; ZDB-GENE-000823-6; hox5b.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR001356; Homeobox.
 DR Pfam; PF00046; homeobox; 1.
 DR PRINTS; PR00024; HOMEBOX.
 DR ProDom; PD000010; Homeobox; 1.
 DR PROSITE; PS00027; HOMEBOX_1; 1.
 DR PROSITE; PS0071; HOMEBOX_2; 1.
 KW DNA-binding; Homeobox; Nuclear protein.
 FT NON_TER 1
 SQ SEQUENCE 43 AA; 5050 MW; 53034C37F3DFA596 CRC64;

Query Match 96.7%; Score 89; DB 13; Length 43;
 Best Local Similarity 93.8%; Pred. No. 5.3e-07;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQIKWIFQNRMRKWKX 16
 Db 10 RQIKWIFQNRMRKWKX 25

RESULT 6
 OS7359 PRELIMINARY; PRT; 46 AA.
 AC OS7359;
 DT 01-MAY-2000 (TRENBLrel. 13, Created)
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)

DE HOXC5A (Fragment).
 GN HOXC5A.
 OS Oryzias latipes (Medaka fish) (Japanese ricefish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
 OC Belontiiformes; Adrianichthyidae; Oryziinae; Oryzias.
 OX NCBI_TaxID=8090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kondo S., Naruse K., Shima A.;
 RT "Hox genes of the medakafish Oryzias latipes."
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
 CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 DR EMBL; AB026960; BA086243.1; -.
 DR HSP; P02833; HMX.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR001356; Homeobox.
 DR Pfam; PF00046; homeobox; 1.
 DR PRINTS; PR00024; HOMEBOX.
 DR ProDom; PD000010; Homeobox; 1.
 DR SMART; SM00389; HMX; 1.
 DR PROSITE; PS00027; HOMEBOX_1; 1.
 DR PROSITE; PS0071; HOMEBOX_2; 1.
 KW DNA-binding; Homeobox; Nuclear protein.
 FT NON_TER 1
 SQ SEQUENCE 46 AA; 5955 MW; 6039999ED4294DD3 CRC64;

Query Match 96.7%; Score 89; DB 13; Length 46;
 Best Local Similarity 93.8%; Pred. No. 5.7e-07;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQIKWIFQNRMRKWKX 16
 Db 23 RQIKWIFQNRMRKWKX 38

RESULT 7
 Q27413 PRELIMINARY; PRT; 51 AA.
 AC Q27413;
 DT 01-NOV-1996 (TRENBLrel. 01, Created)
 DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
 DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
 DE LOX5 ORTHOLOG homeobox (Fragment).
 GN CTS-LOX5.
 OS Ctenodrilus serratus.
 OC Eukaryota; Metazoa; Annelida; Polychaeta; Palpata; Canalipalpata;
 OC Terebellida; Ctenodrilidae; Ctenodrilus.
 OX NCBI_TaxID=40316;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94356262; PubMed=7915607;
 RA Dick M.H., Buss L.W.;
 RT "A PCR-based survey of homeobox genes in Ctenodrilus serratus

RT (Annelida: Polychaeta).";
 RL Mol. Phylogenet. Evol. 3:146-158(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Dick M.H., Buss L.W.;
 RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
 CC -|- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 DR EMBL; U26627; AAC46849.1; -.
 DR EMBL; U26629; AAC46851.1; -.
 DR EMBL; S76226; AAB31777.1; -.
 DR HSSP; P02833; 9ANT.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR001356; Homeobox.
 DR PRINTS; PR00024; HOMEBOX.
 DR PROSITE; PS00031; HTHREPRESSR.
 DR InterPro; IPR000047; HTH_lambrepresr.
 DR Pfam; PF00046; Homeobox_1.
 DR PRINTS; PR00031; HTHREPRESSR.
 DR PROSITE; PS00027; HOMEBOX_1; 1.
 DR PROSITE; PS00027; HOMEBOX_2; 1.
 DR SMART; SMO0389; HOX; 1.
 DR PROSITE; PS00027; HOMEBOX_1; 1.
 DR PROSITE; PS00027; HOMEBOX_2; 1.
 KW DNA-binding; Homeobox; Nuclear protein.
 FT NON_TER 1 1
 FT NON_TER 51 51
 SQ SEQUENCE 51 AA; 6278 MW; 88C8F65161E9A22 CRC64;
 Query Match 96.7%; Score 89; DB 5; Length 51;
 Best Local Similarity 93.8%; Pred. No. 6.3e-07;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 RQKIWFQNRNRMKWK 16
 Db :|||||
 23 RQKIWFQNRNRMKWK 38
 RESULT 8
 Q23743
 ID Q23743 PRELIMINARY; PRT; 51 AA.
 AC Q23743;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Deformed ortholog Homeobox (Fragment).
 GN CTS-DFD.
 OS Ctenodrilus serratus.
 OC Eukaryota; Metazoa; Annelida; Polychaeta; Palpata; Canalipalpata;
 OC Terebellida; Ctenodrilidae; Ctenodrilus.
 OX NCBI_TaxID=40316;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Dick M.H., Buss L.W.;
 RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
 CC -|- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 DR EMBL; U26627; AAC46849.1; -.
 DR EMBL; U26629; AAC46851.1; -.
 DR EMBL; S76226; AAB31777.1; -.
 DR HSSP; P02833; 9ANT.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR001356; Homeobox.
 DR PRINTS; PR00024; HOMEBOX.
 DR PROSITE; PS00031; HTHREPRESSR.
 DR InterPro; IPR000047; HTH_lambrepresr.
 DR Pfam; PF00046; Homeobox_1.
 DR PRINTS; PR00031; HTHREPRESSR.
 DR PROSITE; PS00027; HOMEBOX_1; 1.
 DR PROSITE; PS00027; HOMEBOX_2; 1.
 DR SMART; SMO0389; HOX; 1.
 DR PROSITE; PS00027; HOMEBOX_1; 1.
 DR PROSITE; PS00027; HOMEBOX_2; 1.
 KW DNA-binding; Homeobox; Nuclear protein.
 FT NON_TER 1 1
 FT NON_TER 51 51
 SQ SEQUENCE 51 AA; 6278 MW; 88C8F65161E9A22 CRC64;
 Query Match 96.7%; Score 89; DB 5; Length 51;
 Best Local Similarity 93.8%; Pred. No. 6.3e-07;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 RQKIWFQNRNRMKWK 16
 Db :|||||
 23 RQKIWFQNRNRMKWK 38

[2]
 RN SEQUENCE FROM N.A.
 RA Dick M.H., Buss L.W.;
 RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
 CC -|- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 DR EMBL; U26627; AAC46849.1; -.
 DR EMBL; U26629; AAC46851.1; -.
 DR EMBL; S76226; AAB31777.1; -.
 DR HSSP; P02833; 9ANT.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR001356; Homeobox.
 DR PRINTS; PR00024; HOMEBOX.
 DR PROSITE; PS00031; HTHREPRESSR.
 DR InterPro; IPR000047; HTH_lambrepresr.
 DR Pfam; PF00046; Homeobox_1.
 DR PRINTS; PR00031; HTHREPRESSR.
 DR PROSITE; PS00027; HOMEBOX_1; 1.
 DR PROSITE; PS00027; HOMEBOX_2; 1.
 KW DNA-binding; Homeobox; Nuclear protein.
 FT NON_TER 1 1
 FT NON_TER 51 51
 SQ SEQUENCE 51 AA; 6533 MW; 9EDB50C927FECB5 CRC64;
 Query Match 96.7%; Score 89; DB 5; Length 51;
 Best Local Similarity 93.8%; Pred. No. 6.3e-07;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 RQKIWFQNRNRMKWK 16
 Db :|||||
 23 RQKIWFQNRNRMKWK 38
 RESULT 9
 Q26407
 ID Q26407 PRELIMINARY; PRT; 51 AA.
 AC Q26407;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Cts-Dfd protein (Fragment).
 GN CTS-DFD.
 OS Ctenodrilus serratus.
 OC Eukaryota; Metazoa; Annelida; Polychaeta; Palpata; Canalipalpata;
 OC Terebellida; Ctenodrilidae; Ctenodrilus.
 OX NCBI_TaxID=40316;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Dick M.H., Buss L.W.;
 RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
 CC -|- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 DR EMBL; U26627; AAC46849.1; -.
 DR EMBL; U26629; AAC46851.1; -.
 DR EMBL; S76226; AAB31777.1; -.
 DR HSSP; P02833; 9ANT.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.

GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro: IPR001356; Homeobox.
 DR Pfam: PF00046; homeobox; 1.
 DR PRINTS: PR00024; HOMEBOX.
 DR PROSITE: PS00031; HTHREPRESSR.
 DR ProDom: PD000010; Homeobox; 1.
 DR SMART: SM00389; HOX; 1.
 DR PROSITE: PS00027; HOMEBOX; 1; 1.
 DR PROSITE: PS00071; HOMEBOX; 2; 1.
 KW DNA-binding; Homeobox; Nuclear protein.
 FT NON_TER 1
 SQ SEQUENCE 51 AA; 9533 MW; 9EDB40C92/FBCED5 CRC64;
 Query Match 96.7%; Score 89; DB 5; Length 51;
 Best Local Similarity 93.8%; Pred. No. 6.3e-07;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KQIKWIFQNRMRWKX 16
 :|||||
 Db 23 RQIKWIFQNRMRWKX 38
 RESULT 10
 Q9PVR8 PRELIMINARY; PRT; 57 AA.
 AC Q9PVR8;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE HOXA5A (Fragment).
 GN HOXA5A.
 OS Oryzias latipes (Medaka fish) (Japanese ricefish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percormorpha; Atherinomorpha;
 OC Belontiiformes; Adrianichthyidae; Oryziinae; Oryzias.
 OX NCBI_TaxID=8090;
 RN (1)
 RP SEQUENCE FROM N.A.
 RA Kondo S., Naruse K., Shima A.;
 RT "Hox genes of the medaka fish Oryzias latipes";
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 DR EMBL; AB026961; BA86244.1; -.
 DR HSSP; P02833; 1HOM.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro: IPR001356; Homeobox.
 DR Pfam: PF00046; homeobox; 1.
 DR PRINTS: PR00024; HOMEBOX.
 DR ProDom: PD000010; Homeobox; 1.
 DR SMART: SM00389; HOX; 1.
 DR PROSITE: PS00027; HOMEBOX; 1; 1.
 DR PROSITE: PS00071; HOMEBOX; 2; 1.
 KW DNA-binding; Homeobox; Nuclear protein.
 FT NON_TER 1
 SQ SEQUENCE 57 AA; 6891 MW; 54A6430320F68C04 CRC64;
 Query Match 96.7%; Score 89; DB 13; Length 57;
 Best Local Similarity 93.8%; Pred. No. 7e-07;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KQIKWIFQNRMRWKX 16
 :|||||
 Db 23 RQIKWIFQNRMRWKX 38

FT NON_TER 1
 SQ SEQUENCE 57 AA; 6891 MW; 54A6430320F68C04 CRC64;
 Query Match 96.7%; Score 89; DB 13; Length 57;
 Best Local Similarity 93.8%; Pred. No. 7e-07;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KQIKWIFQNRMRWKX 16
 :|||||
 Db 23 RQIKWIFQNRMRWKX 38
 RESULT 11
 Q9Y188 PRELIMINARY; PRT; 58 AA.
 AC Q9Y188;
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE HBI homeodomain protein (Fragment).
 GN HBI.
 OS Priapulus caudatus.
 OC Eukaryota; Metazoa; Priapulida; Priapulidae; Priapulidae; Priapulidae.
 OX NCBI_TaxID=37621;
 RN (1)
 RP SEQUENCE FROM N.A.
 RA de Rosa R., Grenier J.K., Andreeva T., Cook C.E., Adoutte A., Akam M.,
 RA Carroll S.B., Balavoine G.;
 RT "Hox genes in brachiopods and priapulids and protostome evolution";
 RL Nature 399:772-776(1999).
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 DR EMBL; AF144868; RAD40644.1; -.
 DR HSSP; P02833; 9ANT.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro: IPR001356; Homeobox.
 DR InterPro: IPR000047; HTH_lambrepresr.
 DR Pfam: PF00046; homeobox; 1.
 DR PRINTS: PR00024; HOMEBOX.
 DR ProDom: PD000010; Homeobox; 1.
 DR SMART: SM00389; HOX; 1.
 DR PROSITE: PS00027; HOMEBOX; 1; 1.
 DR PROSITE: PS00071; HOMEBOX; 2; 1.
 KW DNA-binding; Homeobox; Nuclear protein.
 FT NON_TER 1
 SQ SEQUENCE 58 AA; 7323 MW; 572F30DA57C9A613 CRC64;
 Query Match 96.7%; Score 89; DB 5; Length 58;
 Best Local Similarity 93.8%; Pred. No. 7.1e-07;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KQIKWIFQNRMRWKX 16
 :|||||
 Db 24 RQIKWIFQNRMRWKX 39

DT 01-JUN-1998 (TrEMBLrel. 06, Created)
 DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Hoxb7 protein (Fragment).
 GN Hoxb7a OR Hoxb7.
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Prince V.B., Joly L., Ekker M., Ho R.K.;
 RT "Zebrafish hox genes: genomic organization and modified colinear
 expression patterns in the trunk."
 RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
 CC -|- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 DR EMBL: Y14533; CAI74868.1; -.
 DR TRANSFAC: T03635; -.
 DR ZFIN: ZDB-GENE-000329-2; hoxb7a.
 DR GO: GO:0005634; C:nucleus; IEA.
 DR GO: GO:0003700; P:transcription factor activity; IEA.
 DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro: IPR001356; Homeobox.
 DR InterPro: IPR000047; HTH_lambdarepressr.
 DR Pfam: PF000046; homeobox_1.
 DR PRINTS: PR00024; HOMEBOX.
 DR PRINTS: PR00031; HTHREPRESSR.
 DR ProDom: PD000010; Homeobox; 1.
 DR SMART: SM00389; HOX; 1.
 DR PROSITE: PS00027; HOMEBOX_1; 1.
 DR PROSITE: PS00071; HOMEBOX_2; 1.
 DR DNA-binding; Homeobox; Nuclear protein.
 KW NON_TER 1 1
 FT NON_TER 1 1
 SQ SEQUENCE 58 AA; 6863 MW; 41EAF1448DA1E5 CRC64;
 Query Match 96.7%; Score 89; DB 13; Length 58;
 Best Local Similarity 93.8%; Pred. No. 7,le-07;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KQIKWQNRNRKWK 16
 DB 14 RQIKWQNRNRKWK 29
 RESULT 14
 QSWRN9
 ID QSWRN9 PRELIMINARY; PRT; 59 AA.
 AC QSWRN9;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Antennapedia (Fragment).
 GN ANTP.
 OS Lithobius atkinsoni.
 OC Eukaryota; Metazoa; Arthropoda; Myriapoda; Chilopoda;
 OC Pleurostigmophora; Lithosiomorpha; Lithobiidae; Lithobius.

DT 01-JUN-1998 (TrEMBLrel. 06, Created)
 DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Hoxb7 protein (Fragment).
 GN Hoxb7a OR Hoxb7.
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Prince V.B., Joly L., Ekker M., Ho R.K.;
 RT "Zebrafish hox genes: genomic organization and modified colinear
 expression patterns in the trunk."
 RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
 CC -|- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 DR EMBL: Y14533; CAI74868.1; -.
 DR TRANSFAC: T03635; -.
 DR ZFIN: ZDB-GENE-000329-2; hoxb7a.
 DR GO: GO:0005634; C:nucleus; IEA.
 DR GO: GO:0003700; P:transcription factor activity; IEA.
 DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro: IPR001356; Homeobox.
 DR InterPro: IPR000047; HTH_lambdarepressr.
 DR Pfam: PF000046; homeobox_1.
 DR PRINTS: PR00024; HOMEBOX.
 DR PRINTS: PR00031; HTHREPRESSR.
 DR ProDom: PD000010; Homeobox; 1.
 DR SMART: SM00389; HOX; 1.
 DR PROSITE: PS00027; HOMEBOX_1; 1.
 DR PROSITE: PS00071; HOMEBOX_2; 1.
 DR DNA-binding; Homeobox; Nuclear protein.
 KW NON_TER 1 1
 FT NON_TER 1 1
 SQ SEQUENCE 58 AA; 6863 MW; 41EAF1448DA1E5 CRC64;
 Query Match 96.7%; Score 89; DB 13; Length 58;
 Best Local Similarity 93.8%; Pred. No. 7,le-07;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KQIKWQNRNRKWK 16
 DB 14 RQIKWQNRNRKWK 29
 RESULT 14
 QSWRN9
 ID QSWRN9 PRELIMINARY; PRT; 59 AA.
 AC QSWRN9;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Antennapedia (Fragment).
 GN ANTP.
 OS Lithobius atkinsoni.
 OC Eukaryota; Metazoa; Arthropoda; Myriapoda; Chilopoda;
 OC Pleurostigmophora; Lithosiomorpha; Lithobiidae; Lithobius.

RESULT 12
 Q25208
 ID Q25208 PRELIMINARY; PRT; 58 AA.
 AC Q25208;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Antennapedia protein (Fragment).
 GN ANTNAPEDIA.
 OS Junonia coenia (Peacock butterfly) (Precis coenia).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
 OC Papilionoidea; Nymphalidae; Nymphalinae; Junonia.
 OX NCBI_TaxID=39708;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95075456; PubMed=7840822;
 RA Warren R.W., Nagy L., Seale J., Gates J., Carroll S.;
 RT "Evolution of homeotic gene regulation and function in flies and
 butterflies."
 RL Nature 372:458-461(1994).
 CC -|- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 DR EMBL: L42135; AA68461.1; -.
 DR EIR: S58850; S58850.
 DR HSPF: P02833; IHOM.
 DR GO: GO:0005634; C:nucleus; IEA.
 DR GO: GO:0003700; P:transcription factor activity; IEA.
 DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro: IPR001356; Homeobox.
 DR InterPro: IPR000047; HTH_lambdarepressr.
 DR Pfam: PF000046; homeobox_1.
 DR PRINTS: PR00024; HOMEBOX.
 DR PRINTS: PR00031; HTHREPRESSR.
 DR ProDom: PD000010; Homeobox; 1.
 DR SMART: SM00389; HOX; 1.
 DR PROSITE: PS00027; HOMEBOX_1; 1.
 DR PROSITE: PS00071; HOMEBOX_2; 1.
 DR DNA-binding; Homeobox; Nuclear protein.
 KW NON_TER 1 1
 FT NON_TER 1 1
 SQ SEQUENCE 58 AA; 7583 MW; BD69B4875BAE565E CRC64;
 Query Match 96.7%; Score 89; DB 5; Length 58;
 Best Local Similarity 93.8%; Pred. No. 7,le-07;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KQIKWQNRNRKWK 16
 DB 43 RQIKWQNRNRKWK 58
 RESULT 13
 Q57362
 ID Q57362 PRELIMINARY; PRT; 58 AA.
 AC Q57362;

OX NCBI_TaxID=177213;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Hughes C.L., Kaufman T.C.;
 RT "Exploring the myriapod body plan: expression patterns of the ten Hox
 genes in a centipede."
 RL Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 DR EMBL; AF434996; AAL36901.1; -;
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR001356; Homeobox.
 DR InterPro; IPR000047; HTH_lamb_repressr.
 DR Pfam; PF00046; homeobox; 1.
 DR PRINTS; PR00024; HOMEBOX_1.
 DR PRINTS; PR00031; HTHREPRESSR.
 DR ProDom; PD000010; Homeobox; 1.
 DR SMART; SM00389; HOX; 1.
 DR PROSITE; PS00027; HOMEBOX_1; 1.
 DR PROSITE; PS00071; HOMEBOX_2; 1.
 KW DNA-binding; Homeobox; Nuclear protein.
 FT NON_TER 1 1
 SQ SEQUENCE 59 AA; 7093 MW; 9560036CE0D515C1 CRC64;
 Query Match 96.7%; Score 89; DB 5; Length 59;
 Best Local Similarity 93.8%; Pred. No. 7.3e-07;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KQIKIWFQNRMRMKKK 16
 Db 23 RQIKIWFQNRMRMKKK 38
 :|||||
 RESULT 15
 Q9NB42 ID Q9NB42 PRELIMINARY; PRT; 59 AA.
 AC Q9NB42;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Transcription factor deformed (Fragment).
 GN DFD.
 OS Anopheles gambiae (African malaria mosquito).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles.
 OX NCBI_TaxID=7163;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21150895; PubMed=11256376;
 RA Powers T.P., Hogan J., Ke Z., Dymbrowski K., Wang X., Collins F.H.,
 RA Kaufman T.C.;
 RT "Characterization of the Hox cluster from the mosquito Anopheles
 gambiae (Diptera: Culicidae)."
 RL Evol. Dev. 2:311-325 (2000).
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 DR EMBL; AF269155; AAF91400.1; -;

DR HSSP; P02833; LSAN.
 DR GO; GO:0005634; C:nucleus; IEA. factor activity; IEA.
 DR GO; GO:0003700; F:transcription of transcription, DNA-dependent; IEA.
 DR InterPro; IPR001356; Homeobox.
 DR Pfam; PF00046; homeobox; 1.
 DR PRINTS; PR00024; HOMEBOX_1.
 DR ProDom; PD000010; Homeobox; 1.
 DR SMART; SM00389; HOX; 1.
 DR PROSITE; PS00027; HOMEBOX_1; 1.
 DR PROSITE; PS00071; HOMEBOX_2; 1.
 KW DNA-binding; Homeobox; Nuclear protein.
 FT NON_TER 1 1
 SQ SEQUENCE 59 AA; 7621 MW; C38A2505A81D9952 CRC64;
 Query Match 96.7%; Score 89; DB 5; Length 59;
 Best Local Similarity 93.8%; Pred. No. 7.3e-07;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KQIKIWFQNRMRMKKK 16
 Db 43 RQIKIWFQNRMRMKKK 58
 :|||||

Search completed: October 4, 2004, 18:56:27
 Job time : 78.8261 secs

0003/00537

**A FIBRIL-BLOCKING PEPTIDE, A METHOD
FOR PREVENTING FIBRIL FORMATION**

**Fred J. Stevens
Yair Argon
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